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OM protein - protein search, using sw model

Run on: November 25, 2003, 16:39:44 ; Search time 17 Seconds
(without alignments)
597.516 Million cell updates/sec

Title: US-09-666-267B-8
Perfect score: 1149
Sequence: 1 GLSHFCSGVIHVTKVEVA.....LRVQTFNNTTKQBHPDN 216

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1149	100.0	288	1 CD80_HUMAN	P33681 homo sapien
2	738	64.2	299	1 CD80_RABIT	P42070 oryctolagus
3	561	48.8	306	1 CD80_MOUSE	Q00609 mus musculus
4	182	15.8	329	1 CD86_HUMAN	P42081 homo sapien
5	161	14.0	302	1 ICOL_HUMAN	O75144 homo sapien
6	152	13.2	309	1 CD86_MOUSE	P42082 mus musculus
7	150.5	13.1	322	1 ICOL_MOUSE	Q9jhj8 mus musculus
8	140.5	12.2	330	1 CD86_RABIT	P42071 oryctolagus
9	138	12.0	509	1 SHS1_RAT	P97710 r protein-t
10	134.5	11.7	583	1 C166_MOUSE	Q61490 mus musculus
11	133.5	11.6	583	1 C166_HUMAN	Q13740 homo sapien
12	129	11.2	221	1 BRFL_EBV	P03228 Epstein-bar
13	127	11.1	526	1 BUTY_HUMAN	Q13410 homo sapien
14	122.5	10.7	588	1 C166_CHICK	P42292 gallus gall
15	120.5	10.5	513	1 SHS1_MOUSE	P97797 m protein-t
16	120	10.4	506	1 SHS1_BOVIN	O46631 bos tauris
17	119	10.4	524	1 BUTY_MOUSE	Q62556 mus musculus
18	116.5	10.1	1088	1 NCAL_XENLA	P16170 xenopus lae
19	115	10.0	761	1 NCAL_HUMAN	P13592 homo sapien
20	115	10.0	848	1 NCAL_HUMAN	P13591 homo sapien
21	110.5	9.6	321	1 TCB_FLV	P11364 feline leuk
22	110	9.6	398	1 SRB1_HUMAN	O00241 homo sapien
23	109.5	9.5	646	1 MUIB_HUMAN	P43121 homo sapien
24	109.5	9.5	853	1 NCAL_BOVIN	P31836 bos taurus
25	109	9.5	387	1 SRB2_HUMAN	Q9plw8 homo sapien
26	109	9.5	526	1 BUTY_BOVIN	P18892 bos taurus
27	109	9.5	2029	1 LAR_DROME	P16621 drosophila
28	108.5	9.4	365	1 CXAR_MOUSE	P97792 mus musculus
29	107.5	9.4	333	1 AMAL_DROME	P15364 drosophila
30	106.5	9.3	858	1 NCAL_RAT	P13596 rattus norv
31	105	9.1	319	1 A33_HUMAN	Q99795 homo sapien
32	105	9.1	1091	1 NCAL_CHICK	P13590 gallus gall
33	104	9.1	1092	1 NCAL_XENLA	P36335 xenopus lae

34	103.5	9.0	725	1 NCAL_MOUSE	P13594 mus musculus
35	103.5	9.0	1115	1 NCAL_MOUSE	P13595 mus musculus
36	103	9.0	298	1 JAM2_HUMAN	P57087 homo sapien
37	102.5	8.9	503	1 SHS1_HUMAN	P78324 h protein-t
38	102	8.9	1443	1 NEOL_CHICK	Q90610 gallus gall
39	101.5	8.8	403	1 RAGE_MOUSE	Q62151 mus musculus
40	100	8.7	413	1 HEMO_WANSE	P13998 manduca sex
41	99.5	8.7	1338	1 VGR1_HUMAN	P17948 h vascular
42	98.5	8.6	365	1 CXAR_HUMAN	P78310 homo sapien
43	98.5	8.6	1242	1 NPHN_MOUSE	Q9Q297 mus musculus
44	98	8.5	278	1 OX2G_RAT	P04218 rattus norv
45	98	8.5	298	1 JAM1_BOVIN	Q9XT56 bos taurus

ALIGNMENTS

RESULT 1
CD80_HUMAN STANDARD; PRT; 288 AA.
ID AC P33681;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE T lymphocyte activation antigen CD80 precursor (Activation B7-1 antigen) (CTLA-4 counter-receptor B7.1) (B7) (BB1).
GN CD80 OR CD28LG1 OR CD28LG OR LAB7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lymphoid;
RX MEDLINE=90010147; PubMed=2794510;
RA Freeman G.J., Freedman A.S., Segil J.M., Lee G., Whitman J.F., Nadler L.M.;
RT "B7, a new member of the Ig superfamily with unique expression on activated and neoplastic B cells.";
RL J. Immunol. 143:2714-2722(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=92307753; PubMed=1377173;
RA Selvakumar A., Mohanraj B.K., Eddy R.L., Shows T.B., White P.C., Dupont B.;
RT "Genomic organization and chromosomal location of the human gene encoding the B-lymphocyte activation antigen B7.";
RL Immunogenetics 36:175-181(1992).
RN [3]
RP SEQUENCE OF 35-38.
RX MEDLINE=91341422; PubMed=1714935;
RA Freeman G.J., Gray G.S., Gimmi C.D., Lombard D.B., Zhou L.-J., White M., Fingerhuth J.D., Gribben J.G., Nadler L.M.;
RT "Structure, expression, and T cell costimulatory activity of the murine homologue of the human B lymphocyte activation antigen B7.";
RL J. Exp. Med. 174:625-631(1991).
RN [4]
RP CHARACTERIZATION.
RX MEDLINE=95088403; PubMed=7527824;
RA Lanier L.L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S., Okumura K., Ito D., Azuma M.;
RT "CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T cell proliferation, cytokine production, and generation of CTL.";
RL J. Immunol. 154:97-105(1995).
RN [5]
RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 35-234.
RX MEDLINE=20125021; PubMed=10661405;
RA Ikemizu S., Gilbert R.J., Fennelly J.A., Collins A.V., Harlos K., Jones E.Y., Stuart D.I., Davis S.J.;
RT "Structure and dimerization of a soluble form of B7-1.";
RL Immunity 12:51-60(2000).
CC -!- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE


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- DR PIR; I46690; I46690.
DR HSP; P33681; 1DR9.
DR InterPro: IPR007110; Ig-Like.
DR InterPro: IPR003599; Ig.
DR InterPro: IPR003006; Ig_MHC.
DR Pfam: PF00047; Ig; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS0835; IG LIKE; 2.
KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
KW Receptor.
FT SIGNAL 1 32 POTENTIAL.
FT CHAIN 33 299 T LYMPHOCYTE ACTIVATION ANTIGEN CD80.
FT DOMAIN 33 243 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 244 269 POTENTIAL.
FT DOMAIN 265 299 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 33 131 IG-LIKE V-TYPE.
FT DOMAIN 144 225 IG-LIKE C2-TYPE.
FT DISULFID 49 115 POTENTIAL.
FT DISULFID 161 215 POTENTIAL.
FT CARBOHYD 52 52 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 88 88 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 97 97 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 122 122 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 185 185 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 206 206 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 210 210 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 299 AA; 33513 MW; 67442235C91D00 CRC64;

Query Match 64.2%; Score 738; DB 1; Length 299;
Best Local Similarity 63.9%; Pred. No. 2.6e-54;
Matches 133; Conservative 36; Mismatches 39; Indels 0; Gaps 0;

QY 4 HFCGVIHTVKEVATLSGHNVSVEELAQTRIVYQKEKQVLTWMSGDMNIWPEYKN 63
DB 29 HFSGSIQVTKSVKEMALSCDYNISIDELARWRIYQKQVQLSIISGQVEVWEYKN 88

QY 64 RTIFDITNLSIVILALRPSDEGTVECVLVKYEKDAFKREHLAEVTLVKADFPPTPSISD 123
DB 89 RTFPDIINLSLMILALRSDKGTTCVQKNGSFRREHLTVLSIRADFPVPSITD 148

QY 124 FEIPTSNIIRICSTGGFPEPHLSWLEGEELNAINTVSQDPETELYAVSSKLDPNMT 183
DB 149 IGHDPDNVRIKRSAGSGFPEPLAWMEDGEELNAVNTVDQDLDTLYSVSSSELDPNVT 208

QY 184 TNHSCWLIKYGLHRYNOTFNNTKQE 211
DB 209 NHHISVCLIKYGLSVQIFPWSKPKQE 236

RESULT 3
CD80_MOUSE STANDARD; PRT; 306 AA.
ID CD80_MOUSE STANDARD; PRT; 306 AA.
AC Q00609;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE T lymphocyte activation antigen CD80 precursor (Activation B7-1
DE antigen) (B7).
DE CD80 OR B7.
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID:10090;
RN [1]
SEQUENCE FROM N.A.
RP TISSUE=B-cell;
RX MEDLINE=91341422; PubMed=1714935;
RA Gray G.S., Freeman G.J., Gimmi C.D., Lombard D.B., Zhou L.J.,
RA White M., Fingerhuth J.D., Gribben J.G., Nadler L.M.;
RT "Structure, expression, and T cell costimulatory activity of the
RT murine homologue of the human B lymphocyte activation antigen B7.";
RL J. Exp. Med. 174:625-631(1991).
RN [2]

SEQUENCE FROM N.A.
RP TISSUE=B-cell;
RX MEDLINE=91307789; PubMed=7686531;
RA Selvakumar A., White P.C., Dupont B.;
RT "Genomic organization of the mouse B-lymphocyte activation antigen
RT B7.";
RL Immunogenetics 38:292-295(1993).
CC !- FUNCTION: INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL FOR T
CC LYMPHOCYTES ACTIVATION. T CELL PROLIFERATION AND CYTOKINE
CC PRODUCTION IS INDUCED BY THE BINDING OF CD28 OR CTLA-4 TO THIS
CC RECEPTOR.
CC !- SUBCELLULAR LOCATION: Type 1 membrane protein.
CC !- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS, GAMMA
CC INTERFERON STIMULATED MONOCYTES AND NONCIRCULATING B-CELL
CC MALIGNANCIES.
CC !- DEVELOPMENTAL STAGE: EXPRESSED BETWEEN 4 AND 12 HOURS POST-
CC ACTIVATION. PROTEIN WAS DETECTED AT CELL SURFACE AT 24 HOURS AND
CC ITS EXPRESSION WAS MAXIMAL FROM 48 TO 72 HOURS POST-ACTIVATION.
CC !- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC !- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
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CC -----
CC EMBL; X60958; CAA43291.1; -
CC EMBL; L12589; AAA37240.1; ALT_SEQ.
CC EMBL; L12585; AAA37240.1; JOINED.
CC EMBL; L12586; AAA37240.1; JOINED.
CC EMBL; L12587; AAA37240.1; JOINED.
CC EMBL; L12588; AAA37240.1; JOINED.
CC FIR; I49503; I49503.
CC HSP; P33681; 1DR9.
CC MGD; MGI:101775; Cd80.
CC InterPro: IPR007110; Ig-Like.
CC InterPro: IPR003599; Ig.
CC InterPro: IPR003006; Ig_MHC.
CC Pfam; PF00047; Ig; 2.
CC SMART; SM00409; IG; 1.
CC PROSITE; PS0835; IG LIKE; 2.
KW Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
KW Receptor.
FT SIGNAL 1 37 T LYMPHOCYTE ACTIVATION ANTIGEN CD80.
FT CHAIN 38 306 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 38 246 POTENTIAL.
FT TRANSMEM 247 268 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 269 306 IG-LIKE V-TYPE.
FT DOMAIN 38 135 IG-LIKE C2-TYPE.
FT DOMAIN 148 229 IG-HINGE LIKE (POTENTIAL).
FT DOMAIN 227 246 POTENTIAL.
FT DISULFID 54 119 POTENTIAL.
FT DISULFID 165 219 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 93 93 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 99 99 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 189 189 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 210 210 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 214 214 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 306 AA; 34589 MW; 1DBADE0931B84C62 CRC64;

Query Match 48.8%; Score 561; DB 1; Length 306;
Best Local Similarity 50.7%; Pred. No. 1.4e-39;
Matches 104; Conservative 41; Mismatches 58; Indels 2; Gaps 2;

QY 12 VTKEVKEVATLSGHNVSVEELAQTRIVYQKEKQVLTWMSGDMNIWPEYKRTIFDITN 71
DB 42 LSKSVKDKVLLPCRYNSPHEDESDRIYQKDKVLSVIAGLKVYKRTLYDNT- 100
QY 72 NLSIVILALRPSDEGTVECVLVKYEKDAFKREHLAEVTLVKADFPPTPSISDFTPSNI 131

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Db 101 TYSLLILGLVLSDRGTVCVQKRGCTGVYKHLALVKLSIKADFSTENITESGNSADT 160
 QY 132 RRIICSTSGGFPPEHLSWLENGELNAINTVSQDPETELYAVSSKLDFFNMTNHSFMC 191
 Db 161 KRITCFASGGFPKPRFSLWLENGELPGLNTTISQDPESELYTSSQDLFTNHTKCL 220
 QY 192 IKYGLHRLVNQTFNNTTKQSHFPDN 216
 Db 221 IKYGDHVSDFTWKPPDP-PDS 244

RESULT 4

CD86_HUMAN STANDARD; PRT; 329 AA.
 AC P42081; Q13655;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE T lymphocyte activation antigen CD86 precursor (Activation B7-2
 DE antigen) (CTLA-4 counter-receptor B7.2) (B70) (FUN-1) (BU63).
 GN CD86 OR CD28LG2.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=94053735; PubMed=7694363;
 RA Freeman G.J., Gribben J.G., Bousiotis V.A., Ng J.W.,
 RA Restivo V.A., Jr., Lombard L.A., Gray G.S., Nadler L.M.;
 RA "Cloning of B7-2: a CTLA-4 counter-receptor that costimulates human T
 RL cell proliferation.";
 RL Science 262:909-911(1993).
 RN [2]
 RP SEQUENCE OF 7-329 FROM N.A.
 RX MEDLINE=94050123; PubMed=7694153;
 RA Azuma M., Ito D., Yagita K., Okumura K., Phillips J.H.,
 RA Lanier L.L., Somoza C.;
 RL "B70 antigen is a second ligand for CTLA-4 and CD28.";
 RL Nature 366:76-79(1993).
 RN [3]
 RP SEQUENCE OF 7-329 FROM N.A.
 RX MEDLINE=95331831; PubMed=7541777;
 RA Jellis C.L., Wang S.S., Rennett P., Borriello F., Sharpe A.H.,
 RA Green N.R., Gray G.S.;
 RL "Genomic organization of the gene coding for the costimulatory human
 RL B-lymphocyte antigen B7-2 (CD86).";
 RL Immunogenetics 42:85-89(1995).
 RN [4]
 RP CHARACTERIZATION.
 RX MEDLINE=95088403; PubMed=7527824;
 RA Lanier L.L., O'Fallon S., Somoza C., Phillips J.H., Linsley P.S.,
 RA Okumura K., Ito D., Azuma M.;
 RL "CD80 (B7) and CD86 (B70) provide similar costimulatory signals for T
 RL cell proliferation, cytokine production, and generation of CTL.";
 RL J. Immunol. 154:97-105(1995).
 RN [5]
 RP IDENTIFICATION AS CD86.
 RX MEDLINE=94348060; PubMed=7520767;
 RA Engel P., Gribben J.G., Freeman G.J., Zhou L.J., Nozawa Y., Abe M.,
 RA Nadler L.M., Waksia H., Tedder T.F.;
 RL "The B7-2 (B70) costimulatory molecule expressed by monocytes and
 RL activated B lymphocytes is the CD86 differentiation antigen.";
 RL Blood 84:1402-1407(1994).
 CC -!- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL
 CC FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY
 CC BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY
 CC EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS,
 CC SUCH AS DECIDING BETWEEN IMMUNITY AND ENERGY THAT IS MADE BY T
 CC CELLS WITHIN 24 HOURS AFTER ACTIVATION.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- TISSUE SPECIFICITY: EXPRESSED BY ACTIVATED B LYMPHOCYTES AND
 CC MONOCYTES.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -!- DATABASE: NAME=PROW; NOTE=CD guide CD86 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd86.htm".
 CC -----
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 CC -----
 CC EMBL; L25259; AAA58389.1; -;
 CC EMBL; U04343; AAA03814.1; -;
 CC EMBL; U17722; AAA86473.1; -;
 CC EMBL; U17717; AAA86473.1; JOINED.
 CC EMBL; U17718; AAA86473.1; JOINED.
 CC EMBL; U17719; AAA86473.1; JOINED.
 CC EMBL; U17721; AAA86473.1; JOINED.
 CC PIR; A48754; A48754.
 CC PDB; 1I85; 04-APR-01.
 CC Genew; HGNC:1705; CD86.
 CC MIM; 601020; -;
 CC GO; GO:0004872; F:receptor activity; TAS.
 CC GO; GO:0008555; P:immune response; TAS.
 CC GO; GO:0008284; P:positive regulation of cell proliferation; TAS.
 CC InterPro; IPR007110; IG-like.
 CC InterPro; IPR003006; IG_MHC.
 CC InterPro; IPR003596; IG_v.
 CC SMART; SM00406; IGV; 1.
 CC PROSITE; PS50835; IG-LIKE; 1.
 CC PROSITE; PS00290; IG-MHC; FALSE NEG.
 CC Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
 KW Receptor; Polymorphism; 3D-structure.
 FT SIGNAL 1 23 POTENTIAL.
 FT CHAIN 24 329 T LYMPHOCYTE ACTIVATION ANTIGEN CD86.
 FT DOMAIN 24 247 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 248 268 POTENTIAL.
 FT DOMAIN 269 329 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 33 131 IG-LIKE V-TYPE.
 FT DOMAIN 150 225 IG-LIKE C2-TYPE.
 FT DISULFID 40 110 POTENTIAL.
 FT DISULFID 157 218 POTENTIAL.
 FT CARBOHYD 33 33 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 47 47 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 135 135 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 146 146 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 154 154 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 177 177 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 192 192 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT CARBOHYD 213 213 N-LINKED (GLCNAC. .) (POTENTIAL).
 FT VARIANT 310 310 A -> T (in dbSNP:1129055).
 FT CONFLICT 27 27 /FTID=VAR 014650.
 FT SEQUENCE 329 AA; 37696 MW; 65D4F3926889CF7D CRC64;
 SQ
 Query Match 15.8%; Score 182; DB 1; Length 329;
 Best Local Similarity 29.0%; Pred. No. 4.9e-08;
 Matches 60; Conservative 38; Mismatches 71; Indels 38; Gaps 10;
 QY 18 EVATLSC---GHNVSVEELAQTRLYWKEKKWVLTMM----SGDMNIWPEYKNTIFDI 69
 Db 34 ETADLPCCFANSQNSLSLV---VFQDQDELVLNEVLGKEKFDVSHKGTSGTSPD- 89
 QY 70 TNNLSIVILALRPSDEGTVCVVKYKDAFKREHLAEVTLKSVKADFPPTPSISDFEIPTS 129
 Db 90 SDSWTLRHLNQLKDKGLYQCIIHKHKPTGMIRIHQMSNELSVLANFSQPEI----VPIS 145
 QY 130 NTR-----RICTSGGFPPEP-HLSWLENGELNAINTV-----SQDETELYAVS 175

Db 146 NITENVYINLTSSIHGYPEPKMSVL-----LRTKNSTIEYDGMQSKQDNVTELYDVS 200

QY 176 SKLDF---NMNTNHSFMCILIKYGLRV 199

Db 201 ISLSVSFPDVTNMTIFCILEDTKTL 227

RESULT 5

ID ICOL HUMAN STANDARD; PRT; 302 AA.

AC 075144; Q9HD18; Q9NR01;

DT 15-JUL-1999 (Rel. 38, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 15-SEP-2003 (Rel. 42, Last annotation update)

DE ICOS ligand precursor (B7 homolog 2) (B7-H2) (B7-like protein G150)

DE (B7-related protein-1) (B7RP-1).

GN ICOSL OR B7H2 OR B7RP1 OR KIAA0653.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;

RN [1]_

RP SEQUENCE FROM N.A. (ISOFORM 1).

RC TISSUE=Dendritic cell;

RX MEDLINE=20477846; PubMed=11023515;

RA Wang S., Zhu G., Chapoval A.I., Dong H., Tamada K., Ni J., Chen L.;

RT "Costimulation of T cells by B7-H2, a B7-like molecule that binds

RT ICOS";

RL Blood 96:2808-2813(2000).

RN [2]

RP SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.

RC TISSUE=Peripheral blood lymphocytes;

RX MEDLINE=20465019; PubMed=11007762;

RA Yoshinaga S.K., Zhang M., Pistillo J., Horan T., Khare S.D., Miner K.,

RA Sonnenberg M., Boone T., Brankow D., Dai T., Delaney J., Han H.,

RA Hui A., Kohno T., Manoukian R., Whoriskey J.S., Coccia M.A.;

RT "Characterization of a new human B7-related protein: B7RP-1 is the

RT ligand to the co-stimulatory protein ICOS";

RN Int. Immunol. 12:1439-1447(2000).

RN [3]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RC TISSUE=Leukocyte;

RX MEDLINE=20126021; PubMed=10657606;

RA Ling V., Wu P.W., Finnerty H.F., Bean K.M., Spaulding V., Fouser L.A.,

RA Leonard J.P., Hunter S.E., Zollner R., Thomas J.L., Miyashiro J.S.,

RA Jacobs K.A., Collins M.;

RT "Identification of G150, a novel B7-like protein that functionally

RT binds to ICOS receptor";

RL J. Immunol. 164:1653-1657(2000).

RN [4]

RP SEQUENCE FROM N.A.

RC TISSUE=Brain;

RX MEDLINE=98403880; PubMed=9734811;

RA Ishikawa K.-I., Nagase T., Suyama M., Miyajima N., Tanaka A.,

RA Kotani H., Nomura N., Ohara O.;

RT "Prediction of the coding sequences of unidentified human genes. X.

RT The complete sequences of 100 new cDNA clones from brain which can

RT code for large proteins in vitro";

RL DNA Res. 5:169-176(1998).

RN [5]

RP SEQUENCE FROM N.A. (ISOFORM 2).

RA Ling V., Dunussi-Joannopoulos K.;

RT "G150 molecules and uses thereof";

RL Patent number WO0121796, 29-MAR-2001.

CC -!- FUNCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL SURFACE RECEPTOR

CC ICOS. ACTS AS A COSTIMULATORY SIGNAL FOR T-CELL PROLIFERATION AND

CC CYTOKINE SECRETION; INDUCES ALSO B-CELL PROLIFERATION AND

CC DIFFERENTIATION INTO PLASMA CELLS. COULD PLAY AN IMPORTANT ROLE IN

CC MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS

CC WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY CO-

CC STIMULATING MEMORY T-CELL FUNCTION (BY SIMILARITY).

CC -!- SUBCELLULAR LOCATION: Type I membrane protein (By similarity).

CC -!- ALTERNATIVE PRODUCTS:

CC

CC Event-Alternative splicing; Named isoforms=2;

CC Comment=Additional isoforms seem to exist;

CC Name=1;

CC IsoId=075144-1; Sequence=Displayed;

CC Name=2;

CC IsoId=075144-2; Sequence=VSP_002520;

CC -!- TISSUE SPECIFICITY: ISOFORM 1 IS WIDELY EXPRESSED (BRAIN, HEART,

CC KIDNEY, LIVER, LUNG, PANCREAS, PLACENTA, SKELETAL MUSCLE, BONE

CC MARROW, COLON, OVARY, PROSTATE, TESTIS, LYMPH NODES, LEUKOCYTES,

CC SPLEEN, THYMUS AND TONSIL), WHILE ISOFORM 2 IS DETECTED ONLY IN

CC LYMPH NODES, LEUKOCYTES AND SPLEEN.

CC -!- INDUCTION: CONSTITUTIVE EXPRESSION IS FURTHER ENHANCED BY

CC TREATMENT WITH TNF-ALPHA IN PERIPHERAL BLOOD B-CELLS AND

CC MONOCYTES, WHILE IT IS DECREASED IN DENDRITIC CELLS.

CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG

CC SUBFAMILY.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.

CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.

CC -!- CAUTION: Ref.4 sequence differs from that shown in position 300

CC onward for an unknown reason.

CC

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>

CC or send an email to license@isb-sib.ch).

CC

CC EMBL; AF199028; AAF34739.1; -;

CC EMBL; AF289028; AAG01176.1; -;

CC EMBL; AF216749; AAK16241.1; -;

CC EMBL; AB014553; BAA31628.1; ALT_SEQ.

CC EMBL; AX100595; CAC36465.1; -;

CC MIM; 605717; -;

CC GO; GO:0016021; C:integral to membrane; NAS.

CC GO; GO:0003793; F:defense/immunity protein activity; NAS.

CC GO; GO:0005102; F:receptor binding activity; TAS.

CC GO; GO:0042104; P:positive regulation of activated T-cell pro. . .; TAS.

CC GO; GO:0007165; P:signal transduction; NAS.

CC GO; GO:0042110; P:T-cell activation; NAS.

CC InterPro; IPR007110; Ig-like.

CC InterPro; IPR003599; Ig.

CC InterPro; IPR003006; Ig_MHC.

CC Pfam; PF00047; Ig_2.

CC SMART; SM00409; IG_1.

CC PROSITE; PS50835; IG_LIKE; 2.

CC B-cell activation; Immune response; Glycoprotein;

CC Immunoglobulin domain; Signal; Transmembrane; Multigene family;

CC Alternative splicing.

CC SIGNAL 1 18

CC CHAIN 19 302

CC DOMAIN 19 256

CC TRANSMEM 257 277

CC DOMAIN 278 302

CC DOMAIN 19 129

CC DOMAIN 141 227

CC DISULFID 37 113

CC DISULFID 158 216

CC CARBOHYD 70 70

CC CARBOHYD 137 137

CC CARBOHYD 173 173

CC CARBOHYD 186 186

CC CARBOHYD 225 225

CC VARSPLIC 300 302

CC SEQUENCE 302 AA; 33349 MW; 647934E21B5E34A CRC64;

CC /FTID=VSP_002520.

CC

CC Query Match 14.0%; Score 161; DB 1; Length 302;

CC Best Local Similarity 26.4%; Pred. No. 2.5e-06;

CC Matches 57; Conservative 36; Mismatches 95; Indels 28; Gaps 8;

QY 14 KEVKEV----ATLSCG-HNVSVEELAQRIYQV-KEKMWLT----MMSGDMNINPEYKN 63

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Db 23 KEVRAMVGSVLSACPEGRFDNDVYVWQTSKTVTVTHIPQNSLENVDSRYRN 82
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Db 83 RALMSPAGMURGFSLFLNVTQDEQKFCFLVLS-QSLGFQEVLSVEVTLHVAANFSVP 141
QY 120 SIDFEIPTSNIIRIICSTSGGPEPHLSWLENGEELNANTVTSQDPETE-----L 171
Db 142 VVSAPHSODELTFTCTSIINGPRPNVYWKTD-----NSLLDQALQNDTVFLNMRGL 196
QY 172 YAVSSKDLFNMNTTNSHSMCLIKYCHLRVNTQTFNMNT 207
Db 197 YDVVSVLRIARTSPVNIACCIEVLLQNLTVGSQT 232

RESULT 6
CD86 MOUSE STANDARD; PRT; 309 AA.
ID CD86 MOUSE AC P42082;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE T lymphocyte activation antigen CD86 precursor (Activation B7-2
DE antigen) (Early T cell costimulatory molecule-1) (ETC-1).
GN CD86.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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RP SEQUENCE FROM N.A.
RX MEDLINE=94065585; PubMed=7504059;
RA Freeman G.J., Borriello F., Hodges R.J., Reiser H., Gribben J.G.,
RA Ng J.W., Kim J., Goldberg J.M., Hathcock K., Laszio G., Lombard L.A.,
RA Wang S., Gray G.S., Nadler L.M., Sharpe A.H.;
RA "Murine B7-2, an alternative CTLA4 counter-receptor that costimulates
RA T cell proliferation and interleukin 2 production.";
RL J. Exp. Med. 178:2185-2192(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=129;
RA Borriello F., Oliveros J., Freeman G.J., Nadler L.M., Sharpe A.H.;
RA "Differential expression of alternate mb7-2 transcripts.";
RL J. Immunol. 155:5490-5497(1995).
RN [3]
RP SEQUENCE OF 7-309 FROM N.A.
RX MEDLINE=94230971; PubMed=7513726;
RA Chen C., Gault A., Shen L., Nabavi N.;
RA "Molecular cloning and expression of early T cell costimulatory
RA molecule-1 and its characterization as B7-2 molecule.";
RL J. Immunol. 152:4929-4936(1994).
CC -1- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL
CC FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY
CC BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY
CC EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS,
CC SUCH AS DECIDING BETWEEN IMMUNITY AND ENERGY THAT IS MADE BY T
CC CELLS WITHIN 24 HOURS AFTER ACTIVATION.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSED ON ACTIVATED B CELLS.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -1- CAUTION: IT IS UNCERTAIN WHETHER MET-1 OR MET-7 IS THE INITIATOR.
CC
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DR EMBL; U39
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DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE ICOS ligand precursor (B7 homolog 2) (B7-H2) (B7-like protein GI50)
 DE (B7-related protein-1) (B7RP-1) (LICOS).
 GN ICOSL OR B7H2 OR B7RP1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RN SEQUENCE FROM N.A. (ISOFORM 1), AND CHARACTERIZATION.
 RP
 RP TISSUE=Lymphocytes;
 RC MEDLINE=20083495; PubMed=10617205;
 RX Yoshinaga S.K., Whoriskey J.S., Khare S.D., Sarmiento U., Guo J.,
 RA Hoshino T., Shih G., Zhang M., Coccia M.A., Kohno T., Tafuri-Bladt A.,
 RA Brankow D., Campbell P., Chang D., Chiu L., Dai T., Duncan G.,
 RA Elliott G.S., Hui A., McCabe S.M., Scully S., Shahinian A.,
 RA Shaklee C.L., Van G., Mak T.W., Senaldi G.;
 RT "T-cell co-stimulation through B7RP-1 and ICOS.";
 RL Nature 402:827-832(1999).
 RL [2]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RP
 RP TISSUE=Thymus;
 RC MEDLINE=20015817; PubMed=10549624;
 RX Swallow M.W., Wallin J.J., Sha W.C.;
 RA "B7h, a novel costimulatory homolog of B7.1 and B7.2, is induced by
 RT TNFalpha.";
 RL Immunity 11:423-432(1999).
 RN [3]
 RN SEQUENCE FROM N.A. (ISOFORM 1).
 RP
 RP STRAIN=C3H/HeJ; TISSUE=Fetal thymus;
 RC MEDLINE=20126021; PubMed=10657606;
 RX Ling V., Wu P.W., Finnerty H.F., Bean K.M., Spaulding V., Fouser L.A.,
 RA Leonard J.P., Hunter S.E., Zollner R., Thomas J.L., Miyashiro J.S.,
 RA Jacobs K.A., Collins M.;
 RT "Identification of GI50, a novel B7-like protein that functionally
 RT binds to ICOS receptor.";
 RL J. Immunol. 164:1653-1657(2000).
 RN [4]
 RN SEQUENCE FROM N.A. (ISOFORM 2).
 RP
 RP TISSUE=Peripheral blood lymphocytes;
 RC MEDLINE=21286479; PubMed=11390480;
 RX Ling V., Wu P.W., Miyashiro J.S., Marusic S., Finnerty H.F.,
 RA Collins M.;
 RT "Differential expression of inducible costimulator-ligand splice
 RT variants: lymphoid regulation of mouse gi50-b and human gi50
 RT molecules";
 RL J. Immunol. 166:7300-7308(2001).
 RN [5]
 RN SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RP
 RP Ling V., Dunussi-Joannopoulos K.;
 RA "GI50 molecules and uses thereof";
 RT Patent number WO0121796, 29-MAR-2001.
 RL
 CC -!- FUNCTION: LIGAND FOR THE T-CELL-SPECIFIC CELL SURFACE RECEPTOR
 CC ICOS. ACTS AS A COSTIMULATORY SIGNAL FOR T-CELL PROLIFERATION AND
 CC CYTOKINE SECRETION; INDUCES ALSO B-CELL PROLIFERATION AND
 CC DIFFERENTIATION INTO PLASMA CELLS. COULD PLAY AN IMPORTANT ROLE IN
 CC MEDIATING LOCAL TISSUE RESPONSES TO INFLAMMATORY CONDITIONS, AS
 CC WELL AS IN MODULATING THE SECONDARY IMMUNE RESPONSE BY CO-
 CC STIMULATING MEMORY T CELL FUNCTION. DURING PREGNANCY, MAY FUNCTION
 CC TO SKEW THE CYTOKINE OF MATERNAL T-CELLS TOWARD IMMUNOPROTECTIVE
 CC TH2 PHENOTYPE.
 CC
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC
 CC -!- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Comment=Additional isoforms seem to exist;
 CC Name=1;
 CC IsoId=Q9JHJ8-1; Sequence=Displayed;
 CC Name=2; Synonyms=B;
 CC IsoId=Q9JHJ8-2; Sequence=VSP 002521;
 CC
 CC -!- TISSUE SPECIFICITY: ISOFORM 1 HIGHEST EXPRESSION IN LYMPHOID
 CC TISSUES, SUCH AS SPLEEN (MOSTLY IN THE MARGINAL ZONE), LYMPH NODES
 CC (PARTICULARLY IN THE CORTEX AND IN BOTH PRIMARY AND SECONDARY

CC FOLLICLES), THYMUS (PREDOMINANTLY IN THE MEDULLA) AND PEYER'S
 CC PATCHES (MOSTLY IN THE FOLLICLES), LOWER LEVELS IN MANY
 CC NONLYMPHOID TISSUES, SUCH AS BRAIN, KIDNEY, LIVER, LUNG,
 CC SKELETAL MUSCLE AND TESTIS. PRESENT ON FRESHLY ISOLATED SPLENIC B-
 CC CELLS. T-CELLS, DENDRITIC CELLS AND MACROPHAGES. THE EXPRESSION OF
 CC ISOFORM 2 IS RESTRICTED TO HEART, SPLEEN AND KIDNEY.
 CC
 CC -!- DEVELOPMENTAL STAGE: DETECTED EARLY IN EMBRYOGENESIS. IN THE YOLK
 CC SAC AT 11.5 AND 12.5 DPC AND, TO A LESSER EXTENT, IN THE LIVER AT
 CC 14.5 DPC.
 CC
 CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
 CC SUBFAMILY.
 CC
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC
 CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC
 CC EMBL; AF216747; AAF45149.1; -;
 CC EMBL; AF199027; AAF34738.1; -;
 CC EMBL; AX100591; CAC36463.1; -;
 CC EMBL; AX100593; CAC36464.1; -;
 CC EMBL; AF394451; AAK77544.1; -;
 CC MGD; MGI:1354701; Icosl.
 CC GO; GO:0005576; C:extracellular; IDA.
 CC GO; GO:0016021; C:integral to membrane; NAS.
 CC GO; GO:0003793; F:defense/immunity protein activity; NAS.
 CC GO; GO:0005102; F:receptor binding activity; TAS.
 CC GO; GO:0045190; P:isotype switching; NAS.
 CC GO; GO:0042104; P:positive regulation of activated T-cell pro. ; TAS.
 CC GO; GO:0045404; P:positive regulation of interleukin-4 biosyn. ; IMP.
 CC GO; GO:0007165; P:signal transduction; NAS.
 CC GO; GO:0042110; P:T-cell activation; NAS.
 CC InterPro; IPR007110; IG-like.
 CC InterPro; IPR003599; IG.
 CC Pfam; PF00047; ig; 1.
 CC SMART; SM00409; ig; 1.
 CC PROSITE; PS50835; IG LIKE; 2.
 CC B-cell activation; Immune response; Glycoprotein;
 CC Immunoglobulin domain; Signal; Transmembrane; Multigene family;
 CC Alternative splicing.
 CC SIGNAL 1 46 BY SIMILARITY.
 CC CHAIN 47 322 ICOS LIGAND.
 CC DOMAIN 47 277 EXTRACELLULAR (POTENTIAL).
 CC TRANSMEM 278 298 POTENTIAL.
 CC DOMAIN 299 322 CYTOPLASMIC (POTENTIAL).
 CC DOMAIN 49 149 IG-LIKE V-TYPE.
 CC DOMAIN 157 263 IG-LIKE C2-TYPE.
 CC DOMAIN 31 38 POLY-LEU.
 CC DOMAIN 289 292 POLY-ALA.
 CC DISULFID 62 138 POTENTIAL.
 CC DISULFID 185 243 POTENTIAL.
 CC CARBOHYD 71 71 N-LINKED (GLCNAC. .) (POTENTIAL).
 CC CARBOHYD 120 120 N-LINKED (GLCNAC. .) (POTENTIAL).
 CC CARBOHYD 163 163 N-LINKED (GLCNAC. .) (POTENTIAL).
 CC CARBOHYD 200 200 N-LINKED (GLCNAC. .) (POTENTIAL).
 CC CARBOHYD 213 213 N-LINKED (GLCNAC. .) (POTENTIAL).
 CC CARBOHYD 252 252 N-LINKED (GLCNAC. .) (POTENTIAL).
 CC CARBOHYD 265 265 N-LINKED (GLCNAC. .) (POTENTIAL).
 CC VARSPLIC 321 322 HA -> TWAPVPQYDILPRYLMSPLKTRGLP (in
 CC isoform 2).
 CC /FTID=VSP 002521.
 CC R -> H (IN REF. 4 AND 5; CAC36464).
 CC CONFLICT 237 237
 CC SEQUENCE 322 AA; 35960 MW; 55CCBA4AD12E47E6 CRC64;
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Query Match 13.1%; Score 150.5; DB 1; Length 322;
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 Matches 65; Conservative 32; Mismatches 102; Indels 41; Gaps 12;


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QY 2 LSHFC--SGVIHVTEKVEKATLSCGHNVSE-----ELAQTRIYQKEKKWV-----L 48
DB 38 LSSLCAASAEETEGANVGNVLSL-----IDPHRRHNSGLVYVWQIENPEVSYTYL 92
QY 49 TMMSGDMNIWPEYKNTIFDITN-----NLSIVILALRPSDEGTVECVLVKYKADAPKREH 104
DB 93 PVKSPGINVSSYKNGRHLSDLSKMGQNFSLVKNVTPQDTQBFCTCRV--FMNTATELVK 150
QY 105 LAE--VTLVKADFP--SISDFEIPTSNIRIICSTSGGPEPHLSWLENGEELNAIN 160
DB 151 ILIEVVRLRVAANFSTPVISTDSNPGQE--RYTTCMSKNGYPEPNLYWI--NTDLSLD 208
QY 161 TTVSQDP-----ETELVAVSSKLDFTNTHSFMLIKYGHRLVN-----QTFNWNNTK 209
DB 209 TALQNNVTYVNLKGLDYVLSTLRPLWTSRGDVLCCVENVALHQNITSISQAESFTGNNTK 268

RESULT 8
CD86 RABIT STANDARD; PRT; 330 AA.
AC P42071;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE B lymphocyte activation antigen CD86 precursor (Activation B7-2 antigen).
DE antigen).
GN CD86
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
[1]
RN SEQUENCE FROM N.A.
RC STRAIN-B/J X CHBB-HM;
RX MEDLINE=95369849; PubMed=7642234;
RA Isono T., Seto A.;
RT "Cloning and sequencing of the rabbit gene encoding T-cell
RT costimulatory molecules.";
RL Immunogenetics 42:217-220(1995).
CC -!- FUNCTION: RECEPTOR INVOLVED IN THE COSTIMULATORY SIGNAL ESSENTIAL
CC FOR T LYMPHOCYTE PROLIFERATION AND INTERLEUKIN 2 PRODUCTION, BY
CC BINDING CD28 OR CTLA-4. MAY PLAY A CRITICAL ROLE IN THE EARLY
CC EVENTS OF T CELL ACTIVATION AND COSTIMULATION OF NAIVE T CELLS,
CC SUCH AS DECIDING BETWEEN IMMUNITY AND ENERGY THAT IS MADE BY T
CC CELLS WITHIN 24 HOURS AFTER ACTIVATION.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D49842; BAA08642.1; -
DR PIR: I46691; I46691.
DR InterPro: IPR007110; Ig-like.
DR InterPro: IPR003006; Ig_MHC.
DR InterPro: IPR003596; Ig_V.
DR SMART: SM00406; IGV; 1.
DR PROSITE: PS50835; IG LIKE; 1.
DR PROSITE: PS00290; IG_MHC; 1.
DR Immunoglobulin domain; T-cell; Glycoprotein; Signal; Transmembrane;
KW Receptor.
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FT CHAIN 23 330
FT DOMAIN 23 247
FT TRANSMEM 248 268
FT DOMAIN 269 330

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FT DOMAIN 33 127
FT DOMAIN 150 225
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FT CARBOHYD 146 146
FT CARBOHYD 154 154
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FT CARBOHYD 213 213
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Query Match 12.2%; Score 140.5; DB 1; Length 330;
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QY 18 EVATLSCGH-NVSVLELAQTRIYQKEKKWVLTMM-----SGDMNIWPEYKNTIFDITN- 71
DB 34 KTADLPCQFTNSQSRSLSELVVFVWQDERLVLYELFLGKREKPDNDPKYIGRTSFDQESW 93
QY 72 NLSIVILALRPSDEGTVECVLVKYKADAPKREHAEVTLVKADPPTPSISDFEIPTSNI 131
DB 94 NLQHNVOIK--DKGVYQCFVHHRGAKGLVPIYQNSLSVLNFTQBEIT-----LISNI 147
QY 132 RR-----IICSTSGGFPPEPHLSWLENGELNAINTTV-----SQDPETELY--AVSS 176
DB 148 TENSAINLTCSVQGVPEPKMFF---VLKTENATTEYDGVIEKSDQNVTLGYNISIG 203
QY 177 KLDF-NMTNHSFMCLIKYGHRLRVNQTNNWTTKQEHFP 214
DB 204 SITFSDIRNATIYCVL-----QTESTETYSQ-HFP 233

RESULT 9
SHS1 RAT STANDARD; PRT; 509 AA.
AC P97710; O08951; O70426; Q9QW15;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein-tyrosine phosphatase non-receptor type substrate 1 precursor
DE (SHP substrate-1) (SHPs-1) (Inhibitory receptor SHPS-1) (Signal-
DE regulatory protein alpha-1) (Sirp-alpha-1) (Brain Ig-like molecule
DE with tyrosine-based activation motifs) (Bit) (Macrophage fusion
DE receptor) (Macrophage membrane protein MFP150).
GN PTPNS1 OR SHPS1 OR SIRP OR BIT OR MFR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]_TaxID=10116;
RP SEQUENCE FROM N.A., SEQUENCE OF 42-60; 68-91; 128-137; 150-158;
RP 174-189; 192-202; 204-212; 218-237; 259-270; 279-282; 405-415 AND
RP 446-453, N-GLYCOSYLATION, PHOSPHORYLATION ON TYROSINE RESIDUES, AND
RP INTERACTIONS WITH PTPN6 AND PTEN11.
RC TISSUE=Fetal fibroblast;
RX MEDLINE=97098667; PubMed=8943344;
RA Fujioaka Y., Matoraki T., Noguchi T., Iwamatsu A., Yamao T.,
RA Takahashi N., Tsuda M., Takada T., Kasuga M.;
RT "A novel membrane glycoprotein, SHPS-1, that binds the SH2-domain-
RT containing protein tyrosine phosphatase SHP-2 in response to mitogens
RT and cell adhesion.";
RL Mol. Cell. Biol. 16:6887-6899(1996).
RN [2]
RP SEQUENCE FROM N.A., SEQUENCE OF 32-48 AND 446-453, FUNCTION, AND
RP PHOSPHORYLATION ON TYROSINE RESIDUES.
RC STRAIN=Sprague-Dawley; TISSUE=Brain;
RX MEDLINE=97415431; PubMed=9271230;
RA Sano S.-I., Ohnishi H., Omori A., Hasegawa J., Kubota M.;
RT "BIT, an immune antigen receptor-like molecule in the brain.";
RT FEBS Lett. 411:327-334(1997).

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FT CONFLICT 162 162 G -> A (IN REF. 2).
FT CONFLICT 189 189 D -> N* (IN REF. 3).
FT CONFLICT 205 205 N -> L (IN REF. 3; AA SEQUENCE).
FT CONFLICT 209 209 N -> G (IN REF. 3; AA SEQUENCE).
FT CONFLICT 405 405 G -> P (IN REF. 3; AA SEQUENCE).
FT CONFLICT 416 416 E -> F (IN REF. 3; AA SEQUENCE).
FT CONFLICT 418 421 NARE -> EQGN (IN REF. 3; AA SEQUENCE).
FT CONFLICT 450 421 R -> E (IN REF. 3; AA SEQUENCE).
FT CONFLICT 499 499 MISSING (IN REF. 3; AA SEQUENCE).
SQ SEQUENCE 509 AA; 55690 MW; 581E0A4DD429F4 CRC64;

Query Match 12.0%; Score 138; DB 1; Length 509;
Best Local Similarity 25.3%; Pred. No. 0.00038;
Matches 75; Conservative 90; Indels 96; Gaps 20;

QY 3 SHFCSGV-----IHWKEVKV-----ATLSCHNVSVLELAQT-RIYQK-----EKKM 46
DB 23 SCFCAGAGKELVKVQADKSVVAAGDSATLNC-----TVSSLTFTVPGIKWFKGEGQNRSP 78
QY 47 VLTWMSGDMNIWPEYKNRTIFDIT--NNL--STVILALRPSDEGTVCVVKYKEDAFKR 102
DB 79 IYFIDGEH--PRITN--VSDATKNNMDFSCISNVTPEAGTYCV--KFKGIVEP 132
QY 103 EHLAEV-----TLVKADFPPTSPIS--DPEIPTSNIRRICTSGGFPPEP-HLSWLENG 153
DB 133 D--TEIKSGGGTTLVLAKPSPEVSGPDGRSGPGQTVNFTCKSYGSPRNITLKLWLDG 190
QY 154 EELNAINNTVSQPELEYAVSSKLDENMTN--HS-FMCLIKYGH-----197
DB 191 KELSHUETITSSKSNVS--YNISSTVSVKLSPEIDHSRVICEVAHVLEGPLNGTANFSN 249
QY 198 -----RVNOT-----FNW-----NTTKQEHFPDN 216
DB 250 IIRVSPILKITQPLTPASQVNLTCQVKPYKALQNLWLENGLSRTDPEHFTDN 306

RESULT 10
C166 MOUSE STANDARD; PRT; 583 AA.
AC Q61450; Q70136;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE C166 antigen precursor (Activated leukocyte-cell adhesion molecule)
GN (ALCAM) (DM-GRASP protein).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NFS;
RX MEDLINE=97353242; PubMed=9209500;
RA Bowen M.A., Bajorath J., D'Egidio M., Whitney G.S., Palmer D.,
RA Kobay J., Starling G.C., Siadak A.W., Aruffo A.;
RT "Characterization of mouse ALCAM (CD166): the CD6 binding domain is
RT conserved in different homologs (CD166) and mediates cross-species binding."
RL Eur. J. Immunol. 27:1469-1478(1997).
RN [2]
RP SEQUENCE OF 227-583 FROM N.A.
RC STRAIN=BALB/c; Tissue=Brain;
RX MEDLINE=94376084; PubMed=8089660;
RA Kanki J.P., Chang S., Kuwada J.Y.;
RT "The molecular cloning and characterization of potential chick
RT DM-GRASP homologs in zebrafish and mouse."
RL J. Neurobiol. 25:831-845(1994).
CC -1- FUNCTION: CELL ADHESION MOLECULE THAT BINDS TO CD6. INVOLVED IN
CC NEURITE EXTENSION BY NEURONS VIA HETEROPHILIC AND HOMOPHILIC
CC INTERACTIONS. MAY PLAY A ROLE IN THE BINDING OF T AND B CELLS TO
CC ACTIVATED LEUKOCYTES, AS WELL AS IN INTERACTIONS BETWEEN CELLS OF
CC THE NERVOUS SYSTEM.
CC -1- SURCELLULAR LOCATION: Type I membrane protein.
```

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CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U95030; AAC06342.1; -
CC EMBL; L25274; AAA37528.1; -
CC HSSP; Q13740; 1KJC.
CC MGD; MGI:1313266; Alcam.
CC GO; GO:0019897; C:extrinsic to plasma membrane; IDA.
CC GO; GO:0007165; P:signal transduction; IPI.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003599; IG.
CC InterPro; IPR003006; IG_MHC.
CC Pfam; PF00047; IG_5.
CC SMART; SM00409; IG_3.
CC PROSITE; PS00835; IG-LIKE; 4.
CC PROSITE; PS00290; IG_MHC; FALSE NEG.
CC Cell adhesion; Immunoglobulin domain; Glycoprotein; Transmembrane;
CC Repeat; Signal.
FT SIGNAL 1 27 POTENTIAL.
FT CHAIN 28 583 CD166 ANTIGEN.
FT DOMAIN 28 527 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 528 549 POTENTIAL.
FT DOMAIN 550 583 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 28 120 IG-LIKE V-TYPE 1.
FT DOMAIN 125 234 IG-LIKE V-TYPE 2.
FT DOMAIN 245 328 IG-LIKE C2-TYPE 1.
FT DOMAIN 333 409 IG-LIKE C2-TYPE 2.
FT DOMAIN 416 501 IG-LIKE C2-TYPE 3.
FT DISULFID 43 113 POTENTIAL.
FT DISULFID 157 220 POTENTIAL.
FT DISULFID 270 313 POTENTIAL.
FT DISULFID 354 392 POTENTIAL.
FT DISULFID 435 485 POTENTIAL.
FT CARBOHYD 95 95 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 167 167 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 265 265 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 306 306 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 361 361 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 457 457 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 480 480 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 499 499 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 227 232 PSQKT -> AAGIPA (IN REF. 2).
FT CONFLICT 454 454 S -> F (IN REF. 2).
SQ SEQUENCE 583 AA; 65161 MW; E7BAFA8FCA8F9489 CRC64;

Query Match 11.7%; Score 134.5; DB 1; Length 583;
Best Local Similarity 25.2%; Pred. No. 0.00087;
Matches 38; Conservative 34; Mismatches 54; Indels 25; Gaps 7;

QY 59 PEYKQRTIFDITNNLSIVILALRPSDEGTVCVVKYKEDAFKREHLAVTLVSKADFP 118
DB 84 PEYKQ--LSLSENVTLSTANAKISDEKRFVCLVLT-EDNVEAPTLVKV-----FKQ 133
QY 119 PSISDFE-----IPTSNIRRI-ICSTSGGFPPLSWLENGELNAINTVTS-----QD 166
DB 134 PSKPEIVNKAPFLETDLQKGLGDCISRDSYDPGNITWYRNGKVLQPVGEVAILFKKEID 193
QY 167 PTLEYAVSSKLDENMTNTH-----SPMCLIKY 194
DB 194 PGTQLYTVTTSLEYKTKTRSDIQMPETCSVTY 224

RESULT 11
C166_HUMAN STANDARD; PRT; 583 AA.
ID C166_HUMAN
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AC Q13740; O60892;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE CD166 antigen precursor (Activated leukocyte-cell adhesion molecule) (ALCAM).
 DE ALCAM OR MEMD.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95279947; PubMed=7760007;
 RA Bowen M.A., Patel D.D., Li X., Modrell B., Malacko A.R., Wang W.-C., Marquardt H., Neubauer M., Pesando J.M., Francke U., Haynes B.F., Aruffo A.;
 RA "Cloning, mapping, and characterization of activated leukocyte-cell adhesion molecule (ALCAM), a CD6 ligand.";
 RT J. Exp. Med. 181:2213-2220(1995).
 RL [2]
 RP SEQUENCE OF 2-583 FROM N.A.
 RX MEDLINE=98161527; PubMed=9502422;
 RA Degen W.G., van Kempen L.C., Gijzen E.G., van Groningen J.J., van Kooyk Y., Bloemers H.P., Swart G.W.;
 RA "MEMD, a new cell adhesion molecule in metastasizing human melanoma cell lines, is identical to ALCAM (activated leukocyte cell adhesion molecule).";
 RT Am. J. Pathol. 152:805-813(1998).
 RL [3]
 RP CD6-BINDING DOMAINS.
 RX MEDLINE=96420463; PubMed=88231162;
 RA Skonier J.E., Bowen M.A., Emswiler J., Aruffo A., Bajorath J.;
 RA "Recognition of diverse proteins by members of the immunoglobulin superfamily: delineation of the receptor binding site in the human CD6 ligand ALCAM.";
 RT Biochemistry 35:12287-12291(1996).
 RL [4]
 RP 3D-STRUCTURE MODELING OF 28-133.
 RX MEDLINE=96060095; PubMed=8520490;
 RA Bajorath J., Bowen M.A., Aruffo A.;
 RA "Molecular model of the N-terminal receptor-binding domain of the human CD6 ligand ALCAM.";
 RT Protein Sci. 4:1644-1647(1995).
 RL [5]
 CC FUNCTION: CELL ADHESION MOLECULE THAT BINDS TO CD6. INVOLVED IN NEURITE EXTENSION BY NEURONS VIA HETEROPHILIC AND HOMOPHILIC INTERACTIONS. MAY PLAY A ROLE IN THE BINDING OF T AND B CELLS TO ACTIVATED LEUKOCYTES, AS WELL AS IN INTERACTIONS BETWEEN CELLS OF THE NERVOUS SYSTEM.
 CC [6]
 CC SUBCELLULAR LOCATION: Type I membrane protein.
 CC [7]
 CC SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC [8]
 CC SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
 CC [9]
 CC DATABASE: NAME=PROW; NOTE=CD guide CD166 entry;
 CC WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd166.htm".
 CC [10]
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 CC [11]
 CC EMBL: L38608; AAB59499.1; --
 CC EMBL: Y10183; CAA71256.1; --
 CC PIR: I39428; I39428.
 CC PDB: 1KJC; 03-APR-96.
 CC Genew: HGNC:400; ALCAM.
 CC MIM: 601662; --
 CC GO: GO:0005102; F:receptor binding activity; TAS.
 CC GO: GO:0007155; P:cell adhesion; TAS.
 CC GO: GO:0007165; P:signal transduction; TAS.
 CC InterPro: IPR007110; Ig-like.

DR InterPro: IPR003599; Ig.
 DR InterPro: IPR003006; Ig_MHC.
 DR Pfam: PF00047; Ig; 5.
 DR SMART: SM00409; Ig; 3.
 DR PROSITE: PS50835; IG LIKE; 4.
 DR PROSITE: PS00290; IG_MHC; FALSE_NEG.
 KW Cell adhesion; Immunoglobulin domain; Glycoprotein; Transmembrane; Repeat; Signal; 3D-structure; Polymorphism.
 FT SIGNAL 1 27
 FT CHAIN 28 583
 FT DOMAIN 28 527
 FT TRANSMEM 528 549
 FT DOMAIN 550 583
 FT DOMAIN 36 120
 FT DOMAIN 125 234
 FT DOMAIN 245 328
 FT DOMAIN 333 409
 FT DOMAIN 416 501
 FT DISULFID 43 113
 FT DISULFID 157 220
 FT DISULFID 270 313
 FT DISULFID 354 392
 FT DISULFID 435 485
 FT CARBOHYD 91 91
 FT CARBOHYD 95 95
 FT CARBOHYD 167 167
 FT CARBOHYD 265 265
 FT CARBOHYD 306 306
 FT CARBOHYD 361 361
 FT CARBOHYD 457 457
 FT CARBOHYD 480 480
 FT CARBOHYD 499 499
 FT VARIANT 258 258
 FT VARIANT 301 301
 FT STRAND 32 33
 FT STRAND 39 44
 FT STRAND 52 59
 FT TURN 61 62
 FT STRAND 65 71
 FT STRAND 76 78
 FT TURN 84 85
 FT STRAND 86 90
 FT STRAND 95 100
 FT STRAND 110 117
 FT TURN 118 119
 FT STRAND 120 123
 FT STRAND 127 128
 FT STRAND 130 131
 SQ SEQUENCE 583 AA; 65132 MW; E023FB3974A60284 CRC64;
 Query Match 11.6%; Score 133.5; DB 1; Length 583;
 Best Local Similarity 24.5%; Pred. No. 0.0011;
 Matches 37; Conservative 35; Mismatches 54; Indels 25; Gaps 7;
 QY 59 PEYKRTIFDITNNLSIVILALRPSDEGTYECVLKYEKDAFKREHLAEVTLISVKADPT 118
 DB 84 PEYKDR--LNUNSEYTLISINARISDEKRFVCMVLT-EDNVEAPTIVKV-----FKQ 133
 QY 119 PSISDFE-----IPTSNIRRI-ICSTSGGFPFPHLSWLENGLNAINNTV-----SQD 166
 DB 134 PSKPIVSKALPLETEQLKGLGDCISDSYPDGNITWYRNGKVLHPLEGAVVIFPKEND 193
 QY 167 PETELYAVSSKLDFFNMT---TNHSPMCLIKY 194
 DB 194 PVTQLYTMTSTLEYKTKRADIOQMPFTCSVTY 224
 RESULT 12
 BRF1_EBV
 ID BRF1_EBV
 AC P03228; STANDARD; PRT; 221 AA.

```

DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE 33 kDa early protein (p33).
GN BARF1
OS Epstein-Barr virus (strain B95-8) (Human herpesvirus 4).
OC Gammaherpesvirinae; no RNA stage; Herpesviridae;
OC Gammaherpesvirinae; Lymphocryptovirus.
OX NCBI_TaxID=10377;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=84270667; PubMed=6087149;
RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
RA Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
RA Tuffnell P.S., Barrell B.G.;
RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
RL Nature 310:207-211(1984).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=84270667; PubMed=6087149;
RA Baer R., Bankier A.T., Biggin M.D., Deininger P.L., Farrell P.J.,
RA Gibson T.J., Hatfull G., Hudson G.S., Satchwell S.C., Seguin C.,
RA Tuffnell P.S., Barrell B.G.;
RT "DNA sequence and expression of the B95-8 Epstein-Barr virus genome.";
RL Nature 310:207-211(1984).
RN [3]
RP IDENTIFICATION OF PROTEIN.
RX MEDLINE=90059873; PubMed=2555151;
RA Wei M.X., Ooka T.;
RT "A transforming function of the BARF1 gene encoded by Epstein-Barr
RT virus.";
RL EMBO J. 8:2897-2903(1989).
CC -!- FUNCTION: BARF1 HAS TRANSFORMING ACTIVITY.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like domain.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
CC EMBL; V01555; CAA24809.1; -.
DR PIR; B43045; Q0BE48.
DR InterPro; IPR007110; IG-like.
DR PROSITE; PS50835; IG LIKE; 1.
KW Immunoglobulin domain; Early protein; Oncogene.
FT DOMAIN 1 120
SQ SEQUENCE 221 AA; 24471 MW; CAA24D1EA28758E CRC64;

Query Match 11.2%; Score 129; DB 1; Length 221;
Best Local Similarity 27.0%; Pred. No. 0.00077;
Matches 43; Conservative 25; Mismatches 47; Indels 44; Gaps 8;

QY 18 EVATLSCGHNVSEELAQTRIYQK-----EKQVLTWMSGDMNIWPE 60
DB 19 QAVTAFGLGERTVLT-----YWRVSLGPEIEVSWFKLGPGEQVLTGRMHHDV-IFIE 71
QY 61 YKNTIFDI--TNNLISIVILALRPSDEGTYECVVKYKDAFKREHLAEV---TLSV-- 112
DB 72 WPRGPFDIHRSANTFLVVTAAINSHDGNLYCRMKLGTEVTKQEHLSVVKPLTSLVHS 131
QY 113 -KADFTPTSIDFEPTSNIRRIICSTSGGFPPEHLSWL 150
DB 132 ERSQFP-----DFSFLT-----VTCVNAFPHPHVQWL 159

RESULT 13
BUTY_HUMAN
ID BUTY_HUMAN STANDARD; PRT; 526 AA.
AC Q13410;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Butyrophilin precursor (BT).
GN BUTN1 OR BTN.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;

RN RP SEQUENCE FROM N.A.
RX TISSUE=Breast;
RX MEDLINE=96201696; PubMed=8611614;
RA Taylor M.R., Peterson J.A., Ceriani R.L., Couto J.R.;
RT "Cloning and sequence analysis of human butyrophilin reveals a
RT potential receptor function.";
RL Biochim. Biophys. Acta 1306:11-4(1996).
CC -!- FUNCTION: MAY FUNCTION IN THE SECRETION OF MILK-FAT DROPLETS. IT
CC MAY ACT AS A SPECIFIC MEMBRANE-ASSOCIATED RECEPTOR FOR THE
CC ASSOCIATION OF CYTOPLASMIC DROPLETS WITH THE APICAL PLASMA
CC MEMBRANE (BY SIMILARITY).
CC -!- SUBUNIT: SEEMS TO ASSOCIATE WITH XANTHINE DEHYDROGENASE/OXIDASE
CC (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: Type 1 membrane protein.
CC -!- SIMILARITY: BELONGS TO THE IMMUNOGLOBULIN SUPERFAMILY. BTN/MOG
CC SUBFAMILY.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; U39576; AAC50489.1; -.
DR PIR; S70587; S70587.
DR Genew; HGNC:1135; BTN1A1.
DR MIM; 601610; -.
DR GO; GO:0005887; C:integral to plasma membrane; TAS.
DR GO; GO:0004872; F:receptor activity; TAS.
DR InterPro; IPR001870; B302.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR006574; PRY.
DR InterPro; IPR003877; SPRY_receptor.
DR Pfam; PF00047; IG; 1.
DR SMART; PF00622; SPRY; 1.
DR SMART; SM00406; IGV; 1.
DR SMART; SM00589; PRY; 1.
DR PROSITE; PS50835; IG LIKE; 2.
KW Transmembrane; Glycoprotein; Immunoglobulin domain; Signal; Repeat.
FT SIGNAL 1 26
FT CHAIN 27 526
FT DOMAIN 27 242
FT TRANSMEM 243 269
FT DOMAIN 270 526
FT DOMAIN 27 138
FT DOMAIN 148 234
FT CARBOHYD 55 55
FT CARBOHYD 215 215
SQ SEQUENCE 526 AA; 59004 MW; E9EAC0CF8DAF94D5 CRC64;

Query Match 11.1%; Score 127; DB 1; Length 526;
Best Local Similarity 27.5%; Pred. No. 0.0032;
Matches 52; Conservative 33; Mismatches 84; Indels 20; Gaps 10;

QY 16 VKEATLSC--GHNVSVEELAQTRIYQKEKKVLTWMSG---DMNIWPEYKNRTIF--- 67
DB 42 VGEDAELPCRLSPNASEHL-ELRWPRKKVSPAVLVHRDGRGEAQEMPEYGRATLVQD 100
QY 68 -DITNLSIVILALRPSDEGTYECVVKYKDAFKREHLAEVTLVSKADFPPTPSIDFEI 126
DB 101 GIAKGRVALRIRGVSDDDGEYTCF---FREDGSVEEAL--VHLKVAALGSDPHIS-MQV 154
QY 127 PTSNIRRIICSTSGGFPPEHLSW-LENGELNAINTVSQDPETE-LYAVSSKLDENMTT 184
DB 155 QENGEICLECTSGVWPEYQVQWRKSGKEFP--STSESRNPDEGLFTVAASVIIRDTS 212

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- QY 185 NUSFMCCLK 193
Db 213 TRNVSCYIQ 221

RESULT 14

CL166_CHICK STANDARD; PRT; 588 AA.
AC P42292;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE CD166 antigen precursor (SC1 glycoprotein) (DM-GRASP protein) (JC7 protein).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 34-53.
RC TISSUE=Embryo;
RX MEDLINE=920310150; PubMed=1931049;
RA Tanaka H., Matsui T., Agata A., Tomura M., Kubota I.,
RA McFarland K.C., Kohr B., Lee A., Phillips H.S., Shelton D.L.;
RT "Molecular cloning and expression of a novel adhesion molecule, SC1.";
RL Neuron 7:535-545(1991).
RN [2]
RN SEQUENCE FROM N.A.
RX MEDLINE=91337449; PubMed=1873027;
RA Burns F.R., von Kannen S., Guy L., Raper J.A., Kamholz J.,
RA Chang S.;
RT "DM-GRASP, a novel immunoglobulin superfamily axonal surface protein
that supports neurite extension.";
RL Neuron 7:209-220(1991).
RN [3]
RN SEQUENCE FROM N.A., AND SEQUENCE OF 34-52; 87-93; 504-512 AND 569-582.
RC TISSUE=Bursa of fabricius;
RX MEDLINE=92302224; PubMed=1608932;
RA Pourquie O., Corbel C., le Caer J.-P., Rossier J., le Douarin N.M.;
RT "BEN, a surface glycoprotein of the immunoglobulin superfamily, is
expressed in a variety of developing systems.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:5261-5265(1992).
RN [4]
RN POSSIBLE FUNCTION.
RX MEDLINE=92211411; PubMed=1313497;
RA Pourquie O., Hallonet M.E.R., le Douarin N.M.;
RT "Association of BEN glycoprotein expression with climbing fiber
axonogenesis in the avian cerebellum.";
RL J. Neurosci. 12:1548-1557(1992).
CC -!- FUNCTION: HOMOPHILIC ADHESION MOLECULE ASSOCIATED WITH CLIMBING
FIBER AXONEMESIS. SUPPORTS NEURITE EXTENSION.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: EXPRESSED IN A RESTRICTED POPULATION OF AXONS.
CC WITHIN THE SPINAL CORD IT IS LOCALIZED TO AXONS IN THE DORSAL
CC FUNICULUS, MIDLINE FLOOR PLATE CELLS, AND MOTONEURONS. FOUND IN
CC EPITHELIAL, CENTRAL NERVOUS SYSTEM, AND HEMOPOIETIC CELLS. EACH
CC DEVELOPING SYSTEM CARRIES DIFFERENTLY GLYCOSYLATED MOLECULAR FORMS
CC OF BEN
CC -!- DEVELOPMENTAL STAGE: WIDELY EXPRESSED DURING EMBRYONIC
CC DEVELOPMENT.
CC -!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; S63276; AAB20170.1; -.

DR EMBL; M76678; AAA48602.1; -.
DR EMBL; X64301; CAA45579.1; -.
DR PIR; A45254; A45254.
DR PIR; JH0464; JH0464.
DR PIR; JH0506; JH0506.
DR HSP; Q13740; IKJC.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig; 5.
DR SMART; SM00409; Ig; 3.
DR PROSITE; PS00835; IG-LIKE; 4.
DR PROSITE; PS00290; IG_MHC; FALSE NEG.
KW Cell adhesion; Immunoglobulin domain; Glycoprotein; Transmembrane;
KW Repeat; Signal.
FT SIGNAL 1 33
FT CHAIN 34 588
FT DOMAIN 34 532
FT TRANSMEM 533 553
FT DOMAIN 554 588
FT DOMAIN 42 126
FT DOMAIN 131 240
FT DOMAIN 251 333
FT DOMAIN 338 414
FT DOMAIN 421 501
FT DISULFID 49 119
FT DISULFID 163 226
FT DISULFID 276 319
FT DISULFID 359 397
FT DISULFID 440 490
FT CARBOHYD 101 101
FT CARBOHYD 173 173
FT CARBOHYD 199 199
FT CARBOHYD 271 271
FT CARBOHYD 312 312
FT CARBOHYD 366 366
FT CARBOHYD 462 462
FT CARBOHYD 485 485
FT CARBOHYD 504 504
FT CONFLICT 1 10
FT CONFLICT 25 25
FT CONFLICT 112 113
FT CONFLICT 329 329
FT CONFLICT 401 402
SQ SEQUENCE 588 AA; 65726 MW; 2A28612D0164531E CRC64;

Query Match 10.7%; Score 122.5; DB 1; Length 588;
Best Local Similarity 25.7%; Pred. No. 0.0087;
Matches 39; Conservative 32; Mismatches 54; Indels 27; Gaps 8;

QY 59 PEYKRTIFDTNNLSIVILALRPSDEGTGECVLYKYEKDAFKREHLAEVTLVKADPT 118
Db 90 PDYKDR--LSSENVTLSIKNARISDEKRFVCMVLT--EDDVSEETPVVKV-----FKQ 139
QY 119 PS-----ISDFEPTSNIRRI-ICSTSGGFPPEHLSWLENG-----EELNAINTVSQ 165
Db 140 PSQPEILHQADF-LETEKMLGMEGVDRDYPGNGVTWKNGRVLQPVVEVVVILNKVE 198
QY 166 DPETELYAVSSKLDNFMT---TNHSFMCILIKY 194
Db 199 NRSTGLFTMTSSLOQMPYTKEDANAKFTCTIVY 230

RESULT 15

SHSI_MOUSE
ID SHSI_MOUSE STANDARD; PRT; 513 AA.
AC P97797; O08907; O35924; O88555; O88556; P97796; Q8R559; Q9QX57;
AC Q9WTN4;
DT 15-SEP-2003 (Rel. 42, Created)
DT 15-SEP-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Protein-tyrosine phosphatase non-receptor type substrate 1 precursor
(SHP substrate-1) (SHPS-1) (Inhibitory receptor SHPS-1) (Signal-

DE regulatory protein alpha-1) (sirp-alpha-1) (msirp-alpha) (MYD-1
DE antigen) (Brain Ig-like molecule with tyrosine-based activation
DE motif) (Bit) (p84)
GN PTPNS1 OR SHPS1 OR SIRP OR MYD1 OR BIT.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
RC TISSUE=Brain;
RX MEDLINE=97223399; PubMed=9070220;
RA Yamao T., Matozaki T., Amano K., Matsuda Y., Takahashi N., Ochi F.,
RA Fujioke Y., Kasuga M.;
RT "Mouse and human SHPS-1: molecular cloning of cDNAs and chromosomal
RT localization of genes.";
RL Biochem. Biophys. Res. Commun. 231:61-67(1997).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2), AND VARIANTS ALA-29; ARG-67; ARG-91;
RP THR-96; SER-128; PRO-194 AND ASN-224.
RC STRAIN=BALB/c; TISSUE=Brain;
RX MEDLINE=97230468; PubMed=9073522;
RA Ohnishi H., Kubota M., Sano S.-I.;
RT "BIT (Bit) maps to mouse chromosome 2.";
RL Genomics 40:504-506(1997).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), SEQUENCE OF 32-53 AND 422-433
RP (ISOFORM 2), VARIANTS ALA-29; ARG-91; THR-96 AND SER-128,
RC N-GLYCOSYLATION, AND TISSUE SPECIFICITY.
RX STRAIN=BALB/c; TISSUE=Brain, and Cerebellum;
RX MEDLINE=98012243; PubMed=9348339;
RA Comu S., Weng W., Olineky S., Ishwad P., Mi Z., Hempel J., Watkins S.,
RA Lagenaur C.F., Narayanan V.;
RT "The murine P84 neural adhesion molecule is SHPS-1, a member of the
RT phosphatase-binding protein family.";
RL J. Neurosci. 17:8702-8710(1997).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORMS 2 AND 3), VARIANTS ALA-29; ARG-67;
RP PRO-74; ALA-83; 86-TYR-VAL-87; ILE-90; ARG-91; THR-96; ALA-114;
RP ILE-118; SER-128; PRO-194; ASN-224; PHE-351 AND ASP-365,
RC N-GLYCOSYLATION, PHOSPHORYLATION ON TYROSINE RESIDUES, INTERACTION
RP WITH PTPN6, AND TISSUE SPECIFICITY.
RC STRAIN=C57BL/6; TISSUE=Fetal thymus;
RX MEDLINE=98380500; PubMed=9712903;
RA Veillette A., Thibautaud E., Latour S.;
RT "High expression of inhibitory receptor SHPS-1 and its association
RT with protein tyrosine phosphatase SHP-1 in macrophages.";
RL J. Biol. Chem. 273:22719-22728(1998).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3), VARIANTS ALA-29; ARG-67;
RP PRO-74; ALA-83; 86-TYR-VAL-87; ILE-90; ARG-91; THR-96; ALA-114;
RP ILE-118; SER-128; PRO-194; ASN-224; PHE-351 AND ASP-365, AND
RC N-GLYCOSYLATION.
RC STRAIN=129/SvJ, and C57BL/6; TISSUE=Brain, and Liver;
RX MEDLINE=20053880; PubMed=10585853;
RA Sano S.-I., Ohnishi H., Kubota M.;
RT "Gene structure of mouse BIT/SHPS-1.";
RL Biochem. J. 344:667-675(1999).
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 2), AND VARIANTS ALA-29; ARG-67;
RP PRO-74; ALA-83; 86-TYR-VAL-87; ILE-90; ARG-91; THR-96; ALA-114;
RP ILE-118; SER-128; PRO-194; ASN-224; PHE-351 AND ASP-365.
RC STRAIN=ILS, and ISS;
RX MEDLINE=21363810; PubMed=11471062;
RA Ehringer M.A., Thompson J., Conroy O., Xu Y., Yang F., Canniff J.,
RA Beeson M., Gordon L., Bennett B., Johnson T.E., Sikela J.M.;
RT "High-throughput sequence identification of gene coding variants
RT within alcohol-related QTLs.";
RL Mamm. Genome 12:657-663(2001).
RN [7]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT PRO-194.
RC TISSUE=Placenta;
RX Wang H., Chen Z., Ullrich A.;

RT "Epidermal growth factor-induced association of SHP2 with mouse SIRP-
RT alpha.";
RN Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [8]
RP FUNCTION, TISSUE SPECIFICITY, AND DEVELOPMENTAL STAGE.
RX MEDLINE=90152134; PubMed=2303162;
RA Chuang W., Lagenaur C.F.;
RT "Central nervous system antigen P84 can serve as a substrate for
RT neurite outgrowth.";
RL Dev. Biol. 137:219-232(1990).
RN [9]
RP N-GLYCOSYLATION, PHOSPHORYLATION BY JAK2 IN RESPONSE TO GROWTH
RP HORMONE, AND INTERACTIONS WITH JAK2 AND PTPN11.
RX MEDLINE=98175985; PubMed=9507023;
RA Stofega M.R., Wang H., Ullrich A., Carter-Su C.;
RT "Growth hormone regulation of SIRP and SHP-2 tyrosyl phosphorylation
RT and association.";
RL J. Biol. Chem. 273:7112-7117(1998).
RN [10]
RP INTERACTION WITH CD47, AND TISSUE SPECIFICITY.
RX MEDLINE=99091586; PubMed=9872987;
RA Jiang P., Lagenaur C.F., Narayanan V.;
RT "Integrin-associated protein is a ligand for the P84 neural adhesion
RT molecule.";
RL J. Biol. Chem. 274:559-562(1999).
RN [11]
RP INTERACTION WITH FGR.
RX MEDLINE=20130295; PubMed=10662797;
RA Gresham H.D., Dale B.M., Potter J.W., Chang P.W., Vines C.M.,
RA Lowell C.A., Lagenaur C.F., Willman C.L.;
RT "Negative regulation of phagocytosis in murine macrophages by the Src
RT kinase family member, Fgr.";
RL J. Exp. Med. 191:515-528(2000).
CC -!- FUNCTION: Immunoglobulin-like cell surface receptor for CD47. Acts
CC as docking protein and induces translocation of PTPN6
CC PTPN11 and other binding partners from the cytosol to the
CC plasma membrane. Supports adhesion of cerebellar neurons, neurite
CC outgrowth and glial cell attachment. May play a key role in
CC intracellular signaling during synaptogenesis and in synaptic
CC function. Involved in the negative regulation of receptor tyrosine
CC kinase-coupled cellular responses induced by cell adhesion, growth
CC factors or insulin. Mediates negative regulation of phagocytosis,
CC mast cell activation and dendritic cell activation. CD47 binding
CC prevents maturation of immature dendritic cells and inhibits
CC cytokine production by mature dendritic cells (By similarity).
CC -!- SUBUNIT: Binds PTPN11 when tyrosine-phosphorylated, except in
CC macrophages, where it primarily binds PTPN6. Binds GRB2 vitro.
CC Binds FGR. Binds JAK2 irrespective of its phosphorylation status
CC and forms a stable complex. Binds SCAP1 and/or SCAP2. The
CC resulting complex recruits Fyb. Binds PTK2B (By similarity).
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=3;
CC Comment=Additional isoforms seem to exist;
CC Name=1; Synonyms=a;
CC IsoId=P97797-1; Sequence=Displayed;
CC Name=2; Synonyms=a', Large;
CC IsoId=P97797-2; Sequence=VSP_007032;
CC Name=3; Synonyms=b, Small;
CC IsoId=P97797-3; Sequence=VSP_007031;
CC -!- TISSUE SPECIFICITY: Highly expressed in cerebral cortex, brain,
CC spinal cord, cerebellum and spleen, and at much lower levels in
CC kidney, thymus, heart, lung and liver. Within the cerebellum,
CC highly expressed throughout the molecular layer, and in synaptic
CC glomeruli in the granule cell layer. Detected in neurons of the
CC hippocampus and dentate gyrus, and in olfactory bulb. Not detected
CC in Purkinje cells. Highly expressed in the plexiform layers, optic
CC fiber layer and the outer segments of the photoreceptor layer in
CC the retina. Highly expressed in macrophages. Isoform 3 is detected
CC at very low levels in all tissues tested.
CC -!- DEVELOPMENTAL STAGE: Highly expressed in the CNS of embryos from
CC day 7 to 17.
CC -!- PTM: N-glycosylated.

```
CC -|- PTM: Phosphorylated on tyrosine residues.
CC -|- SIMILARITY: Contains 2 immunoglobulin-like C1-type domains.
CC -|- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -----
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CC -----
DR EMBL; D87967; BAA13520.1; -
DR EMBL; D87968; BAA13521.1; -
DR EMBL; D85785; BAA20376.1; -
DR EMBL; U89694; AAB92591.1; -
DR EMBL; AF072543; AAC24886.1; -
DR EMBL; AF072544; AAC24887.1; -
DR EMBL; AB024507; BAA89290.1; -
DR EMBL; AB024500; BAA89290.1; JOINED.
DR EMBL; AB024501; BAA89290.1; JOINED.
DR EMBL; AB024502; BAA89290.1; JOINED.
DR EMBL; AB024503; BAA89290.1; JOINED.
DR EMBL; AB024504; BAA89290.1; JOINED.
DR EMBL; AB024505; BAA89290.1; JOINED.
DR EMBL; AB024506; BAA89290.1; JOINED.
DR EMBL; AB018194; BAA76555.1; -
DR EMBL; AB024507; BAA89289.1; -
DR EMBL; AB024500; BAA89289.1; JOINED.
DR EMBL; AB024501; BAA89289.1; JOINED.
DR EMBL; AB024502; BAA89289.1; JOINED.
DR EMBL; AB024503; BAA89289.1; JOINED.
DR EMBL; AB024504; BAA89289.1; JOINED.
DR EMBL; AB024505; BAA89289.1; JOINED.
DR EMBL; AB024506; BAA89289.1; JOINED.
DR EMBL; AF332079; AAK56107.1; -
DR EMBL; AF332080; AAK56108.1; -
DR EMBL; Y10349; CAA71375.1; -
DR PIR; JCS289; JCS289.
DR MGI; 108563; Ptpnsl.
DR GO; GO:0008580; F:cytoskeletal regulator; IMP.
DR GO; GO:0045309; F:phosphoprotein amino acid binding; IPI.
DR GO; GO:0007015; P:actin filament organization; IMP.
DR GO; GO:0006928; P:cell motility; IMP.
DR GO; GO:0007160; P:cell-matrix adhesion; IMP.
DR InterPro; IPR007110; Ig-like.

Query Match 10.5%; Score 120.5; DB 1; Length 513;
Best Local Similarity 25.9%; Pred. NO. 0.011;
Matches 59; Conservative 42; Mismatches 88; Indels 39; Gaps 15;

QY 3 SHFCGV---THVTKEVEA-----TLSCGHNVSEELAQTRIYWQK---EKKMYL 48
Db 23 SCFCGTGKELKVTQPEKSVVAGDSTVLNC---TLTSLLPVGPDKWYRGVGSRLLI 79
QY 49 TMMSGDMNIWPEYKQRTIFDIT--NNL--SIVILALRPSDEGYECVLKYEKDAFKREH 104
Db 80 YSFTGEH--FPRVTN--VSDATKRNMDPSIRISNVTPEADAGTYCV--KFKGSPSEPT 133
QY 105 L-----AVTISVKADFTPS-ISDFEPTNIRRIICSTGGPPEP-HLSWLENGEEL 156
Db 134 EIQSGGTEVYVLAKPSPEVSGPADRGIPDQKV-NFTCKSHGFSRNITLKWFKDQGL 192
QY 157 NAINTTVSQDPETELYAVSS--KLDFNTTNSFMCLIKYGLRVNQT 202
Db 193 HLETTVPNSGKNVSYNISSTVRLNSMDVHS-KVICEVAHITLDRS 239
```

Search completed: November 25, 2003, 16:45:48

Job time : 42 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 25, 2003, 16:42:47 ; Search time 35 Seconds
(without alignments)

1592.553 Million cell updates/sec

Title: US-09-666-267B-8

Perfect score: 1149

Sequence: 1 GLSHFCSGVIHVTKEVKEVA.....LRVNTFNWNTTKQBHPDN 216

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phase.*
- 10: sp_plant.*
- 11: sp_prodent.*
- 12: sp_virus.*
- 13: sp_vertebrate.*
- 14: sp_unclassified.*
- 15: sp_rvirus.*
- 16: sp_bacteriap.*
- 17: sp_archaeap.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1118	97.3	288	6	O77684 macaca neme
2	1100	95.7	288	6	Q28499 macaca mula
3	1085	94.4	288	6	Q9BDN6 cercocobus
4	1085	94.4	289	6	Q28347 cercocobus
5	772	67.2	296	6	Q8WMZ2 sus scrofa
6	764	66.5	230	6	Q9N213 sus scrofa
7	762.5	66.4	288	6	Q9TT70 sus scrofa
8	762.5	66.4	297	6	Q9BE99 sus scrofa
9	761	66.2	229	6	Q9TT71 sus scrofa
10	743	64.7	292	6	Q9GMZ8 felis silve
11	743	64.7	292	6	O02758 felis silve
12	719	62.6	304	6	Q9TQX1 canis famil
13	717.5	62.4	296	6	O46405 bos taurus
14	705	61.4	235	6	Q9N0T0 canis famil
15	705	61.4	235	6	Q9TQ88 canis famil
16	659	57.4	294	11	Q8BH36 mesocricetu

ALIGNMENTS

RESULT 1

O77684 ID O77684 PRELIMINARY; PRT; 288 AA.
AC O77684;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE B7 protein.
DE B7.
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheidae;
OC Cercopitheidae; Macaca.
OX NCBI_TaxID=9545;
RN [1]
RP SEQUENCE FROM N.A.
RA Kraus G., Hnatyszyn J.H.;
RL Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF079519; AAC31555.1; -
DR HSSP; P33681; IDR9.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; ig, 1.
DR SMART; SM00409; IG, 1.
DR PROSITE; PS00835; IG_LIKE; 2.
SQ SEQUENCE 288 AA; 33131 MW; 76B8C42839E9AB79 CRC64;

Query Match 97.3%; Score 1118; DB 6; Length 288;
Best Local Similarity 97.7%; Pred. No. 1e-92; 4; Indels 0; Gaps 0;
Matches 210; Conservative 1; Mismatches 1;

QY 2 LSHFCSGVIHVTKEVKEVATLSGHNVSVEELAQTRIYQKKEKMWLTWMSGDMNIWPEY 61
|||||
Db 28 LSHFCSGVIHVTKEVKEVATLSGHNVSVEELAQTRIYQKKEKMWLTWMSGDMNIWPEY 87
|||||
QY 62 KNRTIFDITNNLSIVILALRPSDEGYECVWLKYEKDAFKREHLAEVTVSVKADFTPTSI 121
|||||
Db 88 KNRTIFDITNNLSIVILALRPSDEGYECVWLKYEKDAFKREHLAEVTVSVKADFTPTSI 147
|||||

QY 122 SDFEIPSTNIRRIICSTGGFPEPHLSWLENGELNAINTVSQDPETELYAVSSKLDNF 181
Db 148 TDFEIPSPNIRRIICSTGGFPEPHLSWLENGELNAINTVSQDPETELYVSSKLDNF 207
QY 182 MTNHSFMCILIKYGHRLVNTFNWNTTKQEHFPDN 216
Db 208 MTNHSFMCILIKYGHRLVNTFNWNTPKQEHFPDN 242

RESULT 2
Q28499 PRELIMINARY; PRT; 288 AA.
AC Q28499;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE B7 protein (CD80 protein precursor).
GN B7 OR N939.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and nonhuman primates."
RL J. Immunol. 155:3946-3954 (1995).
RN [2]

RP SEQUENCE FROM N.A.
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P., Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing and homology analysis of nonhuman primate Fas/Fas-Ligand and co-stimulatory molecules."
RL Immunogenetics 0:0-0(2001).
DR EMBL; U19840; AAA86706.1; -.
DR EMBL; AF344849; AAK37609.1; -.
DR HSSP; P33681; IDR9.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG-LIKE; 2.
KW Signal.
FT SIGNAL
SQ SEQUENCE 288 AA; 33141 MW; E70BEA4006C7A609 CRC64;

Query Match 95.78; Score 1100; DB 6; Length 288;
Best Local Similarity 96.38; Pred. No. 4.2e-91;
Matches 207; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
QY 2 LSHFCSGVIHVTKEKVEATLSGCHNVSVVEELAQTRIVYQKQKMWLTMSGDMNIWPEY 61
Db 28 LSHFCSGVIHVTKEKVEATLSGCHNVSVVEELAQTRIVYQKQKMWLTMSGDMNIWPEY 87
QY 62 KRTIFDITNLSIVILALRPSDEGYECVVLKYKDAFKREHLAEVTLISKADFTPTSI 121
Db 88 KRTIFDITNLSIVILALRPSDEGYECVVLKYKDAFKREHLAEVTLISKADFTPTSI 147
QY 122 SDFEIPSTNIRRIICSTGGFPEPHLSWLENGELNAINTVSQDPETELYAVSSKLDNF 181
Db 148 TDFEIPSPNIRRIICSTGGFPEPHLSWLENGELNAINTVSQDPETELYVSSKLDNF 207
QY 182 MTNHSFMCILIKYGHRLVNTFNWNTTKQEHFPDN 216
Db 208 MTNHSFMCILIKYGHRLVNTFNWNTPKQEHFPDN 242

RESULT 3
Q9BDN6 PRELIMINARY; PRT; 288 AA.
ID Q9BDN6;
AC Q9BDN6;
DT 01-JUN-2001 (T-EMBLrel. 17, Created)
DT 01-JUN-2001 (T-EMBLrel. 17, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE CD80 protein.
GN MNB71.
OS Cercopithecus torquatus atys (Red-crowned mangabey) (Sooty mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.
OX NCBI_TaxID=9531;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21383618; PubMed=11491535;
RA Villinger F., Bostik P., Mayne A.E., King C.L., Genain C.P., Weiss W.R., Ansari A.A.;
RT "Cloning, sequencing, and homology analysis of nonhuman primate Fas/Fas-Ligand and co-stimulatory molecules."
RL Immunogenetics 53:315-328(2001).
DR EMBL; AF344839; AAK37535.1; -.
DR HSSP; P33681; IDR9.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG-LIKE; 1.
SQ SEQUENCE 288 AA; 32917 MW; C6A3F6A3C592972B CRC64;

Query Match 94.4%; Score 1085; DB 6; Length 288;
Best Local Similarity 95.3%; Pred. No. 9.4e-90;
Matches 205; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY 2 LSHFCSGVIHVTKEKVEATLSGCHNVSVVEELAQTRIVYQKQKMWLTMSGDMNIWPEY 61
Db 28 LSHFCSGVIHVTKEKVEATLSGCHNVSVVEELAQTRIVYQKQKMWLTMSGDMNIWPEY 87
QY 62 KRTIFDITNLSIVILALRPSDEGYECVVLKYKDAFKREHLAEVTLISKADFTPTSI 121
Db 88 KRTIFDITNLSIVILALRPSDEGYECVVLKYKDAFKREHLAEVTLISKADFTPTSI 147
QY 122 SDFEIPSTNIRRIICSTGGFPEPHLSWLENGELNAINTVSQDPETELYAVSSKLDNF 181
Db 148 TDFEIPSPNIRRIICSTGGFPEPHLSWLENGELNAINTVSQDPETELYVSSKLDNF 207
QY 182 MTNHSFMCILIKYGHRLVNTFNWNTTKQEHFPDN 216
Db 208 MTNHSFVCILIKYGHRLVNTFNWNTPKQEHFPDN 242

RESULT 4
Q28347 PRELIMINARY; PRT; 289 AA.
ID Q28347;
AC Q28347;
DT 01-NOV-1996 (T-EMBLrel. 01, Created)
DT 01-NOV-1996 (T-EMBLrel. 01, Last sequence update)
DT 01-MAR-2003 (T-EMBLrel. 23, Last annotation update)
DE B7 protein (Fragment).
GN B7.
OS Cercopithecus torquatus (red-crowned mangabey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciinae; Cercopithecus.
OX NCBI_TaxID=9530;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=96003435; PubMed=7561102;
RA Villinger F., Brar S.S., Mayne A., Chikkala N., Ansari A.A.;
RT "Comparative sequence analysis of cytokine genes from human and

nonhuman primates.";
- RL J. Immunol. 155:3946-3954(1995).
DR EMBL; U19833; AAA86700.1; -;
DR HSSP; P33681; 1DR9.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 1.
FT NON TER 289
SQ SEQUENCE 289 AA; 33030 MW; 5ED6A3F6A3C59297 CRC64;

Query Match 94.4%; Score 1085; DB 6; Length 289;
Best Local Similarity 95.3%; Pred. No. 9.5e-90;
Matches 205; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 2 LSHFCSGVHVTKEVKEVATLSCGHNVSVVEELAQTRIIYQKEKKMVLTMMSGDMNIWPE 61
DB 28 LSHFCSGVHVTKEVKEVATLSCGHNVSVVEELAQTRIIYQKEKKMVLTMMSGDMNIWPE 87

QY 62 KNRITFDIINNLSIVILALRPSDEGTGECVWLKYEKDAFKREHLAEVTLVKADPPTPSI 121
DB 88 KNRITFDIINNLSIVILALRPSDEGTGECVWLKYEKDAFKREHLAEVTLVKADPPTPSI 147

QY 122 SDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDNF 181
DB 148 TDFEIPSPNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDNF 207

QY 182 MTNHSFMCILIKYGHRLVNQTNNTTKOEHPFDN 216
DB 208 MTNHSFVCLIKYGHRLVNQTNNTTKOEHPFDN 242

RESULT 5
Q8WMZ2 PRELIMINARY; PRT; 296 AA.
AC Q8WMZ2;
DT 01-WAR-2002 (TREMBLrel. 20, Created)
DT 01-WAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-WAR-2003 (TREMBLrel. 23, Last annotation update)
DE CD80.
GN CD80.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Tadaki D.K., Williams A., Lee K.P., Kirk A.D., Harlan D.M.;
RT "Porcine CD80: Cloning, characterization and evidence for its role in
direct human T-cell activation";
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF45811; AAL58443.1; -;
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 2.
SQ SEQUENCE 296 AA; 33275 MW; 69E494237E679C98 CRC64;

Query Match 67.2%; Score 772; DB 6; Length 296;
Best Local Similarity 66.8%; Pred. No. 1.6e-61;
Matches 141; Conservative 28; Mismatches 42; Indels 0; Gaps 0;

QY 1 GLSHFCSGVHVTKEVKEVATLSCGHNVSVVEELAQTRIIYQKEKKMVLTMMSGDMNIWPE 60
DB 22 GLDFCSGIVQVTKTKEIAVLSCDYNISTEELTRVRIYQKDNEMVLAVMSGKVKWPK 81

QY 61 YKNRTIFDITNNLSIVILALRPSDEGTGECVWLKYEKDAFKREHLAEVTLVKADPPTPS 120
DB 82 YENRTFTDVTNNLCIVILALRLSDNGTYTCVQKERGSKLEHLTSVKLMVKADFPVPS 141

QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDNF 180
DB 142 ITALGNPSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDNF 201

QY 181 NMTNHSFMCILIKYGHRLVNQTNNTTK 209
DB 202 NVTGNHSFMCILIKYGHRLVNQTNNTTK 230
SQ SEQUENCE 296 AA; 33275 MW; 69E494237E679C98 CRC64;

QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDNF 180
DB 142 ITALGNPSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDNF 201

QY 181 NMTNHSFMCILIKYGHRLVNQTNNTTKOE 211
DB 202 NVTGNHSFMCILIKYGHRLVNQTNNTTKOE 232

RESULT 6
Q9N2I3 PRELIMINARY; PRT; 230 AA.
AC Q9N2I3;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-WAR-2003 (TREMBLrel. 23, Last annotation update)
DE CD80 protein precursor.
GN CD80/B7.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RA Wada M., Amae S., Hoshi M., Nio M., Ohi R.;
RT "Porcine CD80(B-7) mRNA, partial cds";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB026121; BAA90700.2; -;
DR HSSP; P33681; 1DR9.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; IG; 2.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS50835; IG LIKE; 2.
KW Signal.
FT SIGNAL 1 29 POTENTIAL.
FT CHAIN 30 230 POTENTIAL.
SQ SEQUENCE 230 AA; 26028 MW; EB63AD172663C4A4 CRC64;

Query Match 66.5%; Score 764; DB 6; Length 230;
Best Local Similarity 67.0%; Pred. No. 6.2e-61;
Matches 140; Conservative 26; Mismatches 43; Indels 0; Gaps 0;

QY 1 GLSHFCSGVHVTKEVKEVATLSCGHNVSVVEELAQTRIIYQKEKKMVLTMMSGDMNIWPE 60
DB 22 GLDFCSGIVQVTKTKEIAVLSCDYNISTEELTRVRIYQKDNEMVLAVMSGKVKWPK 81

QY 61 YKNRTIFDITNNLSIVILALRPSDEGTGECVWLKYEKDAFKREHLAEVTLVKADPPTPS 120
DB 82 YENRTFTDVTNNLCIVILALRLSDNGTYTCVQKERGSKLEHLTSVKLMVKADFPVPS 141

QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDNF 180
DB 142 ITALGNPSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDNF 201

QY 181 NMTNHSFMCILIKYGHRLVNQTNNTTK 209
DB 202 NVTGNHSFMCILIKYGHRLVNQTNNTTK 230
SQ SEQUENCE 230 AA; 26028 MW; EB63AD172663C4A4 CRC64;

Query Match 66.5%; Score 764; DB 6; Length 230;
Best Local Similarity 67.0%; Pred. No. 6.2e-61;
Matches 140; Conservative 26; Mismatches 43; Indels 0; Gaps 0;

QY 1 GLSHFCSGVHVTKEVKEVATLSCGHNVSVVEELAQTRIIYQKEKKMVLTMMSGDMNIWPE 60
DB 22 GLDFCSGIVQVTKTKEIAVLSCDYNISTEELTRVRIYQKDNEMVLAVMSGKVKWPK 81

QY 61 YKNRTIFDITNNLSIVILALRPSDEGTGECVWLKYEKDAFKREHLAEVTLVKADPPTPS 120
DB 82 YENRTFTDVTNNLCIVILALRLSDNGTYTCVQKERGSKLEHLTSVKLMVKADFPVPS 141

QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDNF 180
DB 142 ITALGNPSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDNF 201

QY 181 NMTNHSFMCILIKYGHRLVNQTNNTTK 209
DB 202 NVTGNHSFMCILIKYGHRLVNQTNNTTK 230
SQ SEQUENCE 230 AA; 26028 MW; EB63AD172663C4A4 CRC64;


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QY 1 GLSHFCGVHVTKEVKEVATLSCGHNVSVVEELAQTRIIYWKQKRVLTVMSCGDMNIWPE 60
DB 22 GLDFDSCGIVQVTKTKETAVLSCDNIISTEELTRVRIYWKQKNEMLVAMSGKVWPK 81
QY 61 YKRTIFDITNLSIVILALRPSDEGTCECVLKYKDAFKREHLAEVTLVKADPTPS 120
DB 82 YENRTTDTVNLCIVILALRSLDNGTYTCVQKRGRGSKYKLEHLTSVKLMVKADFPVPS 141
QY 121 ISDFEIPTSNIRRIICSTSGGFPPEHLSEENLAINNTVTSQDPETELYAVSSKLDNF 180
DB 142 ITALGNPSPNIKRISTSGGFPPEHLSEENLAINNTVTSQDPETELYAVSSKLDNF 201
QY 181 NMTNHSFMCILIKYGHRLVNTQFNW 205
DB 202 NVTGNHSPMCLVKYGLTWSQTNW 226

RESULT 10
Q9GMZ8 PRELIMINARY; PRT; 292 AA.
AC Q9GMZ8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE B-lymphocyte activation antigen B7-1 (CD80).
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20485322; PubMed=11029611;
RA Nishimura Y., Shimajima M., Miyazawa T., Sato E., Nakamura K.,
RA Izumiya Y., Ikeda Y., Mikami T., Takahashi E.,
RT "Molecular cloning of the cDNA encoding the feline B-lymphocyte
RT activation antigen B7-1 (CD80) and B7-2 (CD86) homologues which
RT interact with human CTLA4-Ig."
RL Eur. J. Immunogenet. 27:427-430(2000).
DR EMBL; AB030651; BAB11687.1;
DR HSSP; P33681; 1DR9.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00409; IG_1.
DR PROSITE; PS50835; IG_LIKE; 2.
SQ SEQUENCE 292 AA; 33540 MW; ED9AECE10D30401 CRC64;

Query Match 64.7%; Score 743; DB 6; Length 292;
Best Local Similarity 63.3%; Pred. No. 6.5e-59;
Matches 136; Conservative 33; Mismatches 44; Indels 2; Gaps 1;

QY 2 LSHFCGVHVTKEVKEVATLSCGHNVSVVEELAQTRIIYWKQKRVLTVMSCGDMNIWPEY 61
DB 28 LFYFCGIIQVNTKEEVAVLSCDNIISTEELTRVRIYWKQKDEMLVAMSGKVWPKY 87
QY 62 KNRTIFDITNLSIVILALRPSDEGTCECVLKYKDAFKREHLAEVTLVKADPTPSI 121
DB 88 KNRTFTDVTNLSIVILALRSLDNGTYTCIIQIKEGSKYKHLTSVMLLVRAFPVPSI 147
QY 122 SDFEIPTSNIRRIICSTSGGFPPEHLSEENLAINNTVTSQDPETELYAVSSKLDNF 181
DB 148 TDLGNPESHNIKIMCLTSGGFPKPHLSWLEENLAINNTVTSQDPETELYAVSSKLDNF 207
QY 182 MTNHSFMCILIKYGHRLVNTQFNWNTTKOEHFPDN 216
DB 208 MTNHSFCLVKYGNLLVSQIFNWQ--KSEPQPSN 240

RESULT 11
Q02758 PRELIMINARY; PRT; 292 AA.
ID Q02758

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AC Q02758;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE T-cell specific surface glycoprotein B7-1.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RX Hash S.M., Collison E.W.;
RT "Felis catus t-cell specific surface glycoprotein B7-1."
RL Thesis (1996), Veterinary Pathobiology, Texas A&M Univ.
DR EMBL; U57755; AAB53575.1;
DR HSSP; P33681; 1DR9.
DR InterPro; IPR003599; Ig.
DR InterPro; IPR007110; Ig-like.
DR InterPro; IPR003006; Ig_MHC.
DR Pfam; PF00047; Ig_1.
DR SMART; SM00409; IG_1.
DR PROSITE; PS50835; IG_LIKE; 2.
SQ SEQUENCE 292 AA; 33482 MW; 6F117E7852B7950F CRC64;

Query Match 64.7%; Score 743; DB 6; Length 292;
Best Local Similarity 63.3%; Pred. No. 6.5e-59;
Matches 136; Conservative 33; Mismatches 44; Indels 2; Gaps 1;

QY 2 LSHFCGVHVTKEVKEVATLSCGHNVSVVEELAQTRIIYWKQKRVLTVMSCGDMNIWPEY 61
DB 28 LFYFCGIIQVNTKEEVAVLSCDNIISTEELTRVRIYWKQKDEMLVAMSGKVWPKY 87
QY 62 KNRTIFDITNLSIVILALRPSDEGTCECVLKYKDAFKREHLAEVTLVKADPTPSI 121
DB 88 KNRTFTDVTNLSIVILALRSLDNGTYTCIIQIKEGSKYKHLTSVMLLVRAFPVPSI 147
QY 122 SDFEIPTSNIRRIICSTSGGFPPEHLSEENLAINNTVTSQDPETELYAVSSKLDNF 181
DB 148 TDLGNPESHNIKIMCLTSGGFPKPHLSWLEENLAINNTVTSQDPETELYAVSSKLDNF 207
QY 182 MTNHSFMCILIKYGHRLVNTQFNWNTTKOEHFPDN 216
DB 208 MTNHSFCLVKYGNLLVSQIFNWQ--KSEPQPSN 240

RESULT 12
Q9TOX1 PRELIMINARY; PRT; 304 AA.
AC Q9TOX1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE B7-1 protein precursor.
GN CD80.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20093996; PubMed=10630300;
RA Yang S., Sim G.-K.;
RT "New Forms of Dog CD80 and CD86 Transcripts that Encode Secreted B7
RT Molecules."
RL Immunogenetics 50:349-353(1999).
DR EMBL; AF106824; AAF17295.1;
DR EMBL; AF106833; AAF17293.1;
DR EMBL; AF106829; AAF17293.1; JOINED.
DR EMBL; AF106830; AAF17293.1; JOINED.
DR EMBL; AF106831; AAF17293.1; JOINED.
DR EMBL; AF106832; AAF17293.1; JOINED.
DR HSSP; P33681; 1DR9.
DR InterPro; IPR003599; Ig.

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-OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20093996; PubMed=10630300;
RA Yang S., Sim G.-K.;
RT "New Forms of Dog CD80 and CD86 Transcripts that Encode Secreted B7
  Molecules.";
RL Immunogenetics 50:349-353(1999).
DR EMBL; AF106825; AAF17296.1; -
DR EMBL; AF106831; AAF17294.1; -
DR EMBL; AF106829; AAF17294.1; JOINED.
DR EMBL; AF106830; AAF17294.1; JOINED.
DR HSSP; P33681; IDR9.
DR InterPro; IPR003599; IG.
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; ig; 1.
DR SMART; SM00409; IG; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
KW Signal.
FT SIGNAL
FT CHAIN
SQ SEQUENCE 235 AA; 26917 MW; CC08CAA676BCB40A CRC64;

Query Match 61.4%; Score 705; DB 6; Length 235;
Best Local Similarity 61.5%; Pred. No. 1.3e-55;
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DB 28 LFYFCGIIQVAKTVKEVAULSCDYNISTELMKVRIYQKDEVVLAVTSGQTKVWSKY 87

QY 62 KURTIFDITNNLSIVILALRPDDEGTYECVLKYEKDAFKREHLAEVTLGVKADFPPTSI 121
DB 88 ENRTFADFNNLSIVIMALRLSDNGKYTCIVQKTEKRSYKVKHMTSVMLLRADFPVPSI 147

QY 122 SDPEIPTSNIIRRIICSTGCGFPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLDNF 181
DB 148 TDLGNPSHDIKRIMCSTSGGFPKPHLSWNEEELNAANTTVSQDPDTELYTISSELDNF 207

QY 182 MTNHSFMCCLKYGHILRVNQTENNNTTK 209
DB 208 ITSNSHVFCLVKYGLTVSQIFNQKCK 235

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Job time : 36 secs
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GenCore version 5.1.6
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*OM protein - protein search, using sw model

Run on: November 25, 2003, 16:46:16 ; Search time 30 Seconds
(without alignments)
1327.992 Million cell updates/sec

Title: US-09-666-267B-8

Perfect score: 1149

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Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 673684 seqs, 184443283 residues

Total number of hits satisfying chosen parameters: 673684

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match' 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1149	100.0	288	9	US-09-837-867A-19
5	1149	100.0	288	10	US-09-910-174A-5
6	1149	100.0	288	10	US-09-896-738-10
7	1149	100.0	288	10	US-09-915-789A-15
8	1149	100.0	288	11	US-09-962-969-19
9	1149	100.0	288	11	US-09-350-202-2
10	1149	100.0	288	12	US-10-032-214-278
11	1149	100.0	288	12	US-10-126-088-2
12	1149	100.0	288	12	US-10-041-319-7
13	1149	100.0	288	15	US-10-261-101-2
14	1149	100.0	473	10	US-09-910-059-131
15	1143	99.5	492	10	US-09-845-899A-3

16	1129	98.3	288	12	US-10-032-214-94	Sequence 94, Appl
17	1121	97.6	288	12	US-10-032-214-69	Sequence 69, Appl
18	1121	97.6	288	12	US-10-032-214-82	Sequence 82, Appl
19	1119	97.4	288	12	US-10-032-214-71	Sequence 71, Appl
20	1119	97.4	288	12	US-10-032-214-77	Sequence 77, Appl
21	1119	97.4	288	12	US-10-032-214-225	Sequence 225, App
22	1118	97.3	288	12	US-10-032-214-84	Sequence 84, Appl
23	1116	97.1	288	12	US-10-032-214-76	Sequence 76, Appl
24	1116	97.1	288	12	US-10-032-214-86	Sequence 86, Appl
25	1116	97.1	288	12	US-10-032-214-87	Sequence 87, Appl
26	1116	97.1	288	12	US-10-032-214-286	Sequence 286, App
27	1114	97.0	288	12	US-10-032-214-226	Sequence 226, App
28	1114	97.0	288	12	US-10-032-214-251	Sequence 251, App
29	1113	96.9	288	12	US-10-032-214-90	Sequence 90, Appl
30	1113	96.9	288	12	US-10-032-214-228	Sequence 228, App
31	1113	96.9	288	12	US-10-032-214-250	Sequence 250, App
32	1112	96.8	288	12	US-10-032-214-78	Sequence 78, Appl
33	1112	96.8	288	12	US-10-032-214-248	Sequence 248, App
34	1111	96.7	288	12	US-10-032-214-238	Sequence 238, App
35	1110	96.6	288	12	US-10-032-214-236	Sequence 236, App
36	1109	96.5	288	12	US-10-032-214-88	Sequence 88, Appl
37	1109	96.5	288	12	US-10-032-214-89	Sequence 89, Appl
38	1109	96.5	288	12	US-10-032-214-92	Sequence 92, Appl
39	1109	96.5	288	12	US-10-032-214-249	Sequence 249, App
40	1108	96.4	287	12	US-10-032-214-243	Sequence 243, App
41	1105	96.2	288	12	US-10-032-214-81	Sequence 81, Appl
42	1104	96.1	300	12	US-10-032-214-74	Sequence 74, Appl
43	1104	96.1	300	12	US-10-032-214-232	Sequence 232, App
44	1103	96.0	288	12	US-10-032-214-91	Sequence 91, Appl
45	1103	96.0	288	12	US-10-032-214-229	Sequence 229, App

ALIGNMENTS

RESULT 1

US-09-915-789A-21
; Sequence 21, Application US/09915789A
; Patent No. US20020168762A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Lieping
; TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY
; FILE REFERENCE: 07039-219001
; CURRENT APPLICATION NUMBER: US/09/915,789A
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/220,991
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 226
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-789A-21

Query Match	100.0%	Score 1149	DB 10	Length 226
Best Local Similarity	100.0%	Pred No. 2,4e-102		
Matches 216	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	1	GLSHFCGVIHVTKEVKEVATLSCGHNVSVEELAQTRIIYQKEKKMVLTMGDMNIWPE	60	
Db	11	GLSHFCGVIHVTKEVKEVATLSCGHNVSVEELAQTRIIYQKEKKMVLTMGDMNIWPE	70	
QY	61	YKNRTIFDTNNLSIVILALRSDSEGTVECVLVKEDAFKREHLAEVTLVSKADPTPS	120	
Db	71	YKNRTIFDTNNLSIVILALRSDSEGTVECVLVKEDAFKREHLAEVTLVSKADPTPS	130	
QY	121	ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSODPETELVAVSSKLD	180	
Db	131	ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSODPETELVAVSSKLD	190	
QY	181	NMTNHSFMCLIKYGLRVNQTENWNTTKQEHFPDN	216	

Db 191 NMVTHSFMCILKYCHLRVNTQENWTTKQEHFPDN 226
|||||
RESULT 2
US-08-592-711-2
Sequence 2, Application US/08592711
Publication No. US20020115214A1
GENERAL INFORMATION:
APPLICANT: June, Carl H.
APPLICANT: Thompson, Craig B.
APPLICANT: Nabel, Gary J.
APPLICANT: Gray, Gary S.
APPLICANT: Rennert, Paul D.
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,711
FILING DATE: 26-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/435,816
FILING DATE: 4-MAY-1995
APPLICATION NUMBER: US 08/403,253
FILING DATE: 10-MARCH-1995
APPLICATION NUMBER: US 08/253,964
FILING DATE: 3-JUNE-1994
APPLICATION NUMBER: US 08/073,223
FILING DATE: 4-JUNE-1993
APPLICATION NUMBER: US 08/200,947
FILING DATE: 23-FEB-1994
APPLICATION NUMBER: US 07/864,805
FILING DATE: 7-APR-1992
APPLICATION NUMBER: US 08/247,505
FILING DATE: 23-MAY-1994
APPLICATION NUMBER: US 07/864,866
FILING DATE: 7-APR-1992
APPLICATION NUMBER: US 08/218,155
FILING DATE: 25-MAR-1994
APPLICATION NUMBER: US 07/864,807
FILING DATE: 7-APR-1992
APPLICATION NUMBER: US 07/902,467
FILING DATE: 16-JUNE-1992
APPLICATION NUMBER: US 07/275,433
FILING DATE: 23-NOV-1988
ATTORNEY/AGENT INFORMATION:
NAME: Mandragouras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-002CP4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
FEATURE:
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: FREEDMAN, ARNOLD S.
AUTHORS: SEGIL, JEFFREY M.

; AUTHORS: LEE, GRACE
 ; AUTHORS: WHITMAN, JAMES F.
 ; AUTHORS: NADLER, LEE M.
 ; TITLE: B7, A New Member Of The Ig Superfamily With
 ; TITLE: Unique Expression On Activated And Neoplastic B Cells
 ; JOURNAL: The Journal of Immunology
 ; VOLUME: 143
 ; ISSUE: 8
 ; PAGES: 2714-2722
 ; DATE: 15-OCT-1989
 ; RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
 US-08-592-711-2

 Query Match 100.0%; Score 1149; DB 8; Length 288;
 Best Local Similarity 100.0%; Pred. No. 3.3e-102;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 GLSHFCGVIHVTKEKAVATLSCGHNVSVEELAAQTRIIYQKEKKVLTWMSGDMNIWPE 60
 Db 27 GLSHFCGVIHVTKEKAVATLSCGHNVSVEELAAQTRIIYQKEKKVLTWMSGDMNIWPE 86

 Qy 61 YKNTIFDITNNLSIVILALRPSDEGTGECVWLKYEKDAFKRHLAEVTLVKADPPTPS 120
 Db 87 YKNTIFDITNNLSIVILALRPSDEGTGECVWLKYEKDAFKRHLAEVTLVKADPPTPS 146

 Qy 121 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 180
 Db 147 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 206

 Qy 181 NMTNHSFMCILIKYGLRLVQNTFNWNTTKQEHFPDN 216
 Db 207 NMTNHSFMCILIKYGLRLVQNTFNWNTTKQEHFPDN 242

 Query Match 100.0%; Score 1149; DB 9; Length 288;
 Best Local Similarity 100.0%; Pred. No. 3.3e-102;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 GLSHFCGVIHVTKEKAVATLSCGHNVSVEELAAQTRIIYQKEKKVLTWMSGDMNIWPE 60
 Db 27 GLSHFCGVIHVTKEKAVATLSCGHNVSVEELAAQTRIIYQKEKKVLTWMSGDMNIWPE 86

 Qy 61 YKNTIFDITNNLSIVILALRPSDEGTGECVWLKYEKDAFKRHLAEVTLVKADPPTPS 120
 Db 87 YKNTIFDITNNLSIVILALRPSDEGTGECVWLKYEKDAFKRHLAEVTLVKADPPTPS 146

 Qy 121 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 180
 Db 147 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 206

 Qy 181 NMTNHSFMCILIKYGLRLVQNTFNWNTTKQEHFPDN 216
 Db 207 NMTNHSFMCILIKYGLRLVQNTFNWNTTKQEHFPDN 242

 Query Match 100.0%; Score 1149; DB 9; Length 288;
 Best Local Similarity 100.0%; Pred. No. 3.3e-102;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 GLSHFCGVIHVTKEKAVATLSCGHNVSVEELAAQTRIIYQKEKKVLTWMSGDMNIWPE 60
 Db 27 GLSHFCGVIHVTKEKAVATLSCGHNVSVEELAAQTRIIYQKEKKVLTWMSGDMNIWPE 86

 Qy 61 YKNTIFDITNNLSIVILALRPSDEGTGECVWLKYEKDAFKRHLAEVTLVKADPPTPS 120
 Db 87 YKNTIFDITNNLSIVILALRPSDEGTGECVWLKYEKDAFKRHLAEVTLVKADPPTPS 146

 Qy 121 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 180
 Db 147 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 206

 Qy 181 NMTNHSFMCILIKYGLRLVQNTFNWNTTKQEHFPDN 216
 Db 207 NMTNHSFMCILIKYGLRLVQNTFNWNTTKQEHFPDN 242

 Query Match 100.0%; Score 1149; DB 9; Length 288;
 Best Local Similarity 100.0%; Pred. No. 3.3e-102;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 GLSHFCGVIHVTKEKAVATLSCGHNVSVEELAAQTRIIYQKEKKVLTWMSGDMNIWPE 60
 Db 27 GLSHFCGVIHVTKEKAVATLSCGHNVSVEELAAQTRIIYQKEKKVLTWMSGDMNIWPE 86

 Qy 61 YKNTIFDITNNLSIVILALRPSDEGTGECVWLKYEKDAFKRHLAEVTLVKADPPTPS 120
 Db 87 YKNTIFDITNNLSIVILALRPSDEGTGECVWLKYEKDAFKRHLAEVTLVKADPPTPS 146

 Qy 121 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 180
 Db 147 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 206

 Qy 181 NMTNHSFMCILIKYGLRLVQNTFNWNTTKQEHFPDN 216
 Db 207 NMTNHSFMCILIKYGLRLVQNTFNWNTTKQEHFPDN 242

 Query Match 100.0%; Score 1149; DB 9; Length 288;
 Best Local Similarity 100.0%; Pred. No. 3.3e-102;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 GLSHFCGVIHVTKEKAVATLSCGHNVSVEELAAQTRIIYQKEKKVLTWMSGDMNIWPE 60
 Db 27 GLSHFCGVIHVTKEKAVATLSCGHNVSVEELAAQTRIIYQKEKKVLTWMSGDMNIWPE 86

 Qy 61 YKNTIFDITNNLSIVILALRPSDEGTGECVWLKYEKDAFKRHLAEVTLVKADPPTPS 120
 Db 87 YKNTIFDITNNLSIVILALRPSDEGTGECVWLKYEKDAFKRHLAEVTLVKADPPTPS 146

 Qy 121 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 180
 Db 147 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 206

 Qy 181 NMTNHSFMCILIKYGLRLVQNTFNWNTTKQEHFPDN 216
 Db 207 NMTNHSFMCILIKYGLRLVQNTFNWNTTKQEHFPDN 242

 Query Match 100.0%; Score 1149; DB 9; Length 288;
 Best Local Similarity 100.0%; Pred. No. 3.3e-102;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 GLSHFCGVIHVTKEKAVATLSCGHNVSVEELAAQTRIIYQKEKKVLTWMSGDMNIWPE 60
 Db 27 GLSHFCGVIHVTKEKAVATLSCGHNVSVEELAAQTRIIYQKEKKVLTWMSGDMNIWPE 86

 Qy 61 YKNTIFDITNNLSIVILALRPSDEGTGECVWLKYEKDAFKRHLAEVTLVKADPPTPS 120
 Db 87 YKNTIFDITNNLSIVILALRPSDEGTGECVWLKYEKDAFKRHLAEVTLVKADPPTPS 146

 Qy 121 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 180
 Db 147 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 206

 Qy 181 NMTNHSFMCILIKYGLRLVQNTFNWNTTKQEHFPDN 216
 Db 207 NMTNHSFMCILIKYGLRLVQNTFNWNTTKQEHFPDN 242

 Query Match 100.0%; Score 1149; DB 9; Length 288;
 Best Local Similarity 100.0%; Pred. No. 3.3e-102;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 GLSHFCGVIHVTKEKAVATLSCGHNVSVEELAAQTRIIYQKEKKVLTWMSGDMNIWPE 60
 Db 27 GLSHFCGVIHVTKEKAVATLSCGHNVSVEELAAQTRIIYQKEKKVLTWMSGDMNIWPE 86

 Qy 61 YKNTIFDITNNLSIVILALRPSDEGTGECVWLKYEKDAFKRHLAEVTLVKADPPTPS 120
 Db 87 YKNTIFDITNNLSIVILALRPSDEGTGECVWLKYEKDAFKRHLAEVTLVKADPPTPS 146

 Qy 121 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 180
 Db 147 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 206

 Qy 181 NMTNHSFMCILIKYGLRLVQNTFNWNTTKQEHFPDN 216
 Db 207 NMTNHSFMCILIKYGLRLVQNTFNWNTTKQEHFPDN 242

 Query Match 100.0%; Score 1149; DB 9; Length 288;
 Best Local Similarity 100.0%; Pred. No. 3.3e-102;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 GLSHFCGVIHVTKEKAVATLSCGHNVSVEELAAQTRIIYQKEKKVLTWMSGDMNIWPE 60
 Db 27 GLSHFCGVIHVTKEKAVATLSCGHNVSVEELAAQTRIIYQKEKKVLTWMSGDMNIWPE 86

 Qy 61 YKNTIFDITNNLSIVILALRPSDEGTGECVWLKYEKDAFKRHLAEVTLVKADPPTPS 120
 Db 87 YKNTIFDITNNLSIVILALRPSDEGTGECVWLKYEKDAFKRHLAEVTLVKADPPTPS 146

 Qy 121 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 180
 Db 147 ISDFEIPTSNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 206

 Qy 181 NMTNHSFMCILIKYGLRLVQNTFNWNTTKQEHFPDN 216
 Db 207 NMTNHSFMCILIKYGLRLVQNTFNWNTTKQEHFPDN 242

 Query Match 100.0%; Score 1149; DB 9; Length 288;
 Best Local Similarity 100.0%; Pred. No. 3.3e-102;
 Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

 Qy 1 GLSHFCGVIHVTKEKAVATLSCGHNVSVEELAAQTRIIYQKEKKVLTWMSGDMNIWPE 60
 Db 27 GLSHFCGVIHVTKEKAVATLSCGHNVSVEELAAQTRIIYQKEKKVLTWMSGDMNIWPE 86

 Qy 61 YKNTIFDITNNLSIVILALRPSDEGTGECVWLKYEKDAFKRHLAEVTLVKADPPTPS 120
 Db 87 YKNTIFDITNNLSIVILALRPSDEGTGECVWLKYEKDAFK

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-910-174A-5

Query Match      100.0%; Score 1149; DB 10; Length 288;
Best Local Similarity 100.0%; Pred. No. 3.3e-102;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIIYQKEKKWVLTMMSGDMNIWPE 60
Db 27 GLSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIIYQKEKKWVLTMMSGDMNIWPE 86

Qy 61 YKNRTIFDITNNLSIVILALRPSDEGYECVVLKYKDAFKREHLAEVTLVKADPPTPS 120
Db 87 YKNRTIFDITNNLSIVILALRPSDEGYECVVLKYKDAFKREHLAEVTLVKADPPTPS 146

Qy 121 ISDFEIPTSNIRRIICSTSGGFPPEHLWENGEELNAINTTVSQDPETELYAVSSKLD 180
Db 147 ISDFEIPTSNIRRIICSTSGGFPPEHLWENGEELNAINTTVSQDPETELYAVSSKLD 206

Qy 181 NMTTNHSMCLIKYGHRLRVNQTNNWTTKQEHFPDN 216
Db 207 NMTTNHSMCLIKYGHRLRVNQTNNWTTKQEHFPDN 242

RESULT 6
US-09-896-738-10
; Sequence 10, Application US/09896738
; Patent No. US20020165347A1
; GENERAL INFORMATION:
; APPLICANT: Fox, Michael
; APPLICANT: Sullivan, John K.
; FILE OF INVENTION: B7-Like Molecules and Uses Thereof
; CURRENT APPLICATION NUMBER: US/09/896,738
; CURRENT FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: 60/215,645
; PRIOR FILING DATE: 2000-06-30
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-896-738-10

Query Match      100.0%; Score 1149; DB 10; Length 288;
Best Local Similarity 100.0%; Pred. No. 3.3e-102;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIIYQKEKKWVLTMMSGDMNIWPE 60
Db 27 GLSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIIYQKEKKWVLTMMSGDMNIWPE 86

Qy 61 YKNRTIFDITNNLSIVILALRPSDEGYECVVLKYKDAFKREHLAEVTLVKADPPTPS 120
Db 87 YKNRTIFDITNNLSIVILALRPSDEGYECVVLKYKDAFKREHLAEVTLVKADPPTPS 146

Qy 121 ISDFEIPTSNIRRIICSTSGGFPPEHLWENGEELNAINTTVSQDPETELYAVSSKLD 180
Db 147 ISDFEIPTSNIRRIICSTSGGFPPEHLWENGEELNAINTTVSQDPETELYAVSSKLD 206

Qy 181 NMTTNHSMCLIKYGHRLRVNQTNNWTTKQEHFPDN 216
Db 207 NMTTNHSMCLIKYGHRLRVNQTNNWTTKQEHFPDN 242

RESULT 7
US-09-915-789A-15
; Sequence 15, Application US/09915789A
; Patent No. US20020168762A1
; GENERAL INFORMATION:
```

```
; APPLICANT: Chen, Lieping
; TITLE OF INVENTION: B7-H3 AND B7-H4, NOVEL IMMUNOREGULATORY
; MOLECULES
; FILE REFERENCE: 07039-219001
; CURRENT APPLICATION NUMBER: US/09/915,789A
; CURRENT FILING DATE: 2002-06-04
; PRIOR APPLICATION NUMBER: US 60/220,991
; PRIOR FILING DATE: 2000-07-27
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15
; LENGTH: 288
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-915-789A-15

Query Match      100.0%; Score 1149; DB 10; Length 288;
Best Local Similarity 100.0%; Pred. No. 3.3e-102;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GLSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIIYQKEKKWVLTMMSGDMNIWPE 60
Db 27 GLSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIIYQKEKKWVLTMMSGDMNIWPE 86

Qy 61 YKNRTIFDITNNLSIVILALRPSDEGYECVVLKYKDAFKREHLAEVTLVKADPPTPS 120
Db 87 YKNRTIFDITNNLSIVILALRPSDEGYECVVLKYKDAFKREHLAEVTLVKADPPTPS 146

Qy 121 ISDFEIPTSNIRRIICSTSGGFPPEHLWENGEELNAINTTVSQDPETELYAVSSKLD 180
Db 147 ISDFEIPTSNIRRIICSTSGGFPPEHLWENGEELNAINTTVSQDPETELYAVSSKLD 206

Qy 181 NMTTNHSMCLIKYGHRLRVNQTNNWTTKQEHFPDN 216
Db 207 NMTTNHSMCLIKYGHRLRVNQTNNWTTKQEHFPDN 242

RESULT 8
US-09-962-969-19
; Sequence 19, Application US/09962969
; Publication No. US20030045703A1
; GENERAL INFORMATION:
; APPLICANT: Sharpe, Sharpe
; Borriello, Francescopaolo
; Freeman, Gordon
; Nadler, Lee
; TITLE OF INVENTION: No. US20030045703A1el Forms of T Cell Costimulatory
; MOLECULES and Uses Therefor
; NUMBER OF SEQUENCES: 65
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 28 State Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII Text
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/962,969
; FILING DATE: 24-Sep-2001
; APPLICATION NUMBER: 08/702,525
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Mandragouras, Amy E.
; REGISTRATION NUMBER: 36,207
; REFERENCE/DOCKET NUMBER: BWI-120CPUS
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
```

TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 19:
US-09-962-969-19

Query Match 100.0%; Score 1149; DB 11; Length 288;
Best Local Similarity 100.0%; Pred. No. 3.3e-102; Indels 0; Gaps 0;
Matches 216; Conservative 0; Mismatches 0;

QY 1 GLSHFCGVIHVTKEVATLSGHNVSVEELAQTRIVYQKEKQAVLTMMSGDMMNWP 60
DB 27 GLSHFCGVIHVTKEVATLSGHNVSVEELAQTRIVYQKEKQAVLTMMSGDMMNWP 86
QY 61 YKNTTFIDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLVKADPPTPS 120
DB 87 YKNTTFIDITNNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLVKADPPTPS 146
QY 121 ISDFRPTNIRITCTSGGPEPHLSWLENCEELNAINTTVSQDPETELYAVSSKLP 180
DB 147 ISDFRPTNIRITCTSGGPEPHLSWLENCEELNAINTTVSQDPETELYAVSSKLP 206
QY 181 NMTNHSFCLIKYGLHVRVQTFNWNNTTKQEHFPDN 216
DB 207 NMTNHSFCLIKYGLHVRVQTFNWNNTTKQEHFPDN 242

RESULT 9
US-09-350-202-2
Sequence 2, Application US/09350202
Publication No. US20030099643A1
GENERAL INFORMATION:
APPLICANT: June, Carl H., Thompson, Craig B., Nabel, Gary J.
APPLICANT: Gray, Gary S., Rennert, Paul D.
TITLE OF INVENTION: Methods For Selectively Stimulating Proliferation Of T-Cells
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 28 State Street
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/350,202
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/403,253
FILING DATE: March 10, 1995
APPLICATION NUMBER: US 08/253,964
FILING DATE: 3 JUNE 1994
APPLICATION NUMBER: US 08/073,223
FILING DATE: 4 JUNE 1993
APPLICATION NUMBER: US 08/200,947
FILING DATE: 23 FEB 1994
APPLICATION NUMBER: US 07/864,805
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/247,505
FILING DATE: 23 MAY 1994
APPLICATION NUMBER: US 07/864,866
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 08/218,155
FILING DATE: 25 MAR 1994

APPLICATION NUMBER: US 07/864,807
FILING DATE: 7 APR 1992
APPLICATION NUMBER: US 07/902,467
FILING DATE: 16 JUNE 1992
APPLICATION NUMBER: US 07/275,433
FILING DATE: 23 NOV 1988
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoras, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-002CP2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
DESCRIPTION: for CD28 T cell surface antigen; transmembrane protein
FEATURE:
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of
IDENTIFICATION METHOD: soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:

NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig V-set domain
LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 185 to 202
IDENTIFICATION METHOD: similarity with known
IDENTIFICATION METHOD: sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J.
AUTHORS: SEGIL, JEFFREY M.
AUTHORS: LEE, GRACE
AUTHORS: WHITMAN, JAMES F.
AUTHORS: NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With
TITLE: Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262

Query Match 100.0%; Score 1149; DB 11; Length 288;
Best Local Similarity 100.0%; Pred. No. 3.3e-102;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIYQKEKKMVLTMMSGDMNIWPE 60
Db 27 GLSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIYQKEKKMVLTMMSGDMNIWPE 86
QY 61 YKNTIFDITNNLSIVILALRPSDEGTVECVLVKYEKDAFKREHLAEVTLVKADPPTPS 120
Db 87 YKNTIFDITNNLSIVILALRPSDEGTVECVLVKYEKDAFKREHLAEVTLVKADPPTPS 146
QY 121 ISDFEIPTSNIRRIICSTSGGFPPEHLSWLENGEELNAINTTVSQDPETELYAVSSKLDLF 180
Db 147 ISDFEIPTSNIRRIICSTSGGFPPEHLSWLENGEELNAINTTVSQDPETELYAVSSKLDLF 206
QY 181 NMTNHSFMCLIKYGHRLRVNQTNNWTTKQEHFPDN 216
Db 207 NMTNHSFMCLIKYGHRLRVNQTNNWTTKQEHFPDN 242

RESULT 10
US-10-032-214-278
Sequence 278, Application US/10032214
Publication No. US20030138881A1
GENERAL INFORMATION:
APPLICANT: FUNNEN, JUHA
APPLICANT: LAZETIC, ALEXANDRA
APPLICANT: LEONG, STEVEN R.
APPLICANT: CHANG, CHIA-CHUN
APPLICANT: APT, DORIS
APPLICANT: GUSTAFSSON, CLAES
TITLE OF INVENTION: NOVEL CO-STIMULATORY MOLECULES
FILE REFERENCE: 02-106730US
CURRENT APPLICATION NUMBER: US/10/032,214
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: 09/888,324

PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: PCT/US01/19973
PRIOR FILING DATE: 2001-06-22
PRIOR APPLICATION NUMBER: 60/213,946
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: 60/241,245
PRIOR FILING DATE: 2000-10-17
NUMBER OF SEQ ID NOS: 320
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 278
LENGTH: 288
TYPE: PRT
ORGANISM: Homo sapiens
US-10-032-214-278
Query Match 100.0%; Score 1149; DB 12; Length 288;
Best Local Similarity 100.0%; Pred. No. 3.3e-102;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIYQKEKKMVLTMMSGDMNIWPE 60
Db 27 GLSHFCGVIHVTKEVATLSCGHNVSVEELAQTRIYQKEKKMVLTMMSGDMNIWPE 86
QY 61 YKNTIFDITNNLSIVILALRPSDEGTVECVLVKYEKDAFKREHLAEVTLVKADPPTPS 120
Db 87 YKNTIFDITNNLSIVILALRPSDEGTVECVLVKYEKDAFKREHLAEVTLVKADPPTPS 146
QY 121 ISDFEIPTSNIRRIICSTSGGFPPEHLSWLENGEELNAINTTVSQDPETELYAVSSKLDLF 180
Db 147 ISDFEIPTSNIRRIICSTSGGFPPEHLSWLENGEELNAINTTVSQDPETELYAVSSKLDLF 206
QY 181 NMTNHSFMCLIKYGHRLRVNQTNNWTTKQEHFPDN 216
Db 207 NMTNHSFMCLIKYGHRLRVNQTNNWTTKQEHFPDN 242
RESULT 11
US-10-126-088-2
Sequence 2, Application US/10126088
Publication No. US20030170821A1
GENERAL INFORMATION:
APPLICANT: FREEMAN, GORDON J.
NADLER, LEE M.
TITLE OF INVENTION: DNA Encoding B7, A New Member
Of The Ig Superfamily With Unique Expression On
Activated And Neoplastic B Cells.
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: The Dana-Farber Cancer Institute
STREET: 44 Binney Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02115
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720kb storage
COMPUTER: IBM Personal System 2; Model 30
OPERATING SYSTEM: MS/DOS
SOFTWARE: WordPerfect 5.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/126,088
FILING DATE: 19-Apr-2002
CLASSIFICATION: <Unknown>
ERIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/751,306
FILING DATE: 28-AUG-1991
APPLICATION NUMBER: US 07/591,300
FILING DATE: 01-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: HART, JULIA D.
REGISTRATION NUMBER: 33132
REFERENCE/DOCKET NUMBER: DFCI-116.1

TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 255-8900
TELEFAX: (203) 259-2846
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 288 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: B cell activation antigen; natural ligand
FEATURE:
NAME/KEY: signal sequence
LOCATION: -34 to -1
IDENTIFICATION METHOD: amino terminal sequencing of soluble protein
OTHER INFORMATION: hydrophobic
FEATURE:
NAME/KEY: extracellular domain
LOCATION: 1 to 208
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: transmembrane domain
LOCATION: 209 to 235
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: intracellular domain
LOCATION: 236 to 254
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 19 to 21
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 55 to 57
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 64 to 66
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 152 to 154
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 173 to 175
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 177 to 179
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 192 to 194
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: N-linked glycosylation
LOCATION: 198 to 200
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: Ig V-set domain

LOCATION: 1 to 104
IDENTIFICATION METHOD: similarity with known sequence
FEATURE:
NAME/KEY: Ig C-set domain
LOCATION: 105 to 202
IDENTIFICATION METHOD: similarity with known sequence
PUBLICATION INFORMATION:
AUTHORS: FREEMAN, GORDON J., FREEDMAN, ARNOLD S. SEGIL, JEFFREY M., LEE, GRACE, WHITMAN, JAMES F. NADLER, LEE M.
TITLE: B7, A New Member Of The Ig Superfamily With Unique Expression On Activated And Neoplastic B Cells
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-126-088-2
Query Match 100.0%; Score 1149; DB 12; Length 288;
Best Local Similarity 100.0%; Pred. No. 3.3e-102;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELACTRIYWOKEKKWLTMMSGDMNIWPE 60
DB 27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELACTRIYWOKEKKWLTMMSGDMNIWPE 86
QY 61 YKNRTIFDITNNLSIVILALRPSDEGTVECVLVKYEKDAFKREHLAEVTLGVKADFPPTPS 120
DB 87 YKNRTIFDITNNLSIVILALRPSDEGTVECVLVKYEKDAFKREHLAEVTLGVKADFPPTPS 146
QY 121 ISDPEIPTSNIIRIICSTSGGFPPEPHLSWLNGLNGEELNAINITVSDPETELVAVSSKLD 180
DB 147 ISDPEIPTSNIIRIICSTSGGFPPEPHLSWLNGLNGEELNAINITVSDPETELVAVSSKLD 206
QY 181 NMTNHSFMCILIKYGLRNVQNTENWNTTKQEHFPDN 216
DB 207 NMTNHSFMCILIKYGLRNVQNTENWNTTKQEHFPDN 242
RESULT 12
US-10-041-319-7
Sequence 7, Application US/10041319
Publication No. US20030180309A1
GENERAL INFORMATION:
APPLICANT: Immunex Corporation
APPLICANT: Baum, Peter R.
APPLICANT: DuBose, Robert F.
TITLE OF INVENTION: HUMAN B7 POLYPEPTIDES
FILE REFERENCE: 3176-A
CURRENT APPLICATION NUMBER: US/10/041.319
CURRENT FILING DATE: 2002-01-07
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patent in version 3.1
SEQ ID NO 7
LENGTH: 288
TYPE: PRT
ORGANISM: Homo sapiens
US-10-041-319-7
Query Match 100.0%; Score 1149; DB 12; Length 288;
Best Local Similarity 100.0%; Pred. No. 3.3e-102;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELACTRIYWOKEKKWLTMMSGDMNIWPE 60
DB 27 GLSHFCSGVIHVTKEVKEVATLSCGHNVSVEELACTRIYWOKEKKWLTMMSGDMNIWPE 86

Qy 61 YKRTIFDITNNLSIVILALRPSDEGTVECVLKYEKDAFKREHLAEVTLVKADPPTPS 120
Db 87 YKRTIFDITNNLSIVILALRPSDEGTVECVLKYEKDAFKREHLAEVTLVKADPPTPS 146
Qy 121 ISDFEIPSTNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 180
Db 147 ISDFEIPSTNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 206
Qy 181 NMTNHSFMCLIKYGHRLVQNTFNWNTTKQEHFPDN 216
Db 207 NMTNHSFMCLIKYGHRLVQNTFNWNTTKQEHFPDN 242

RESULT 13

US-10-261-101-2
GENERAL INFORMATION:
APPLICANT: Ostrand-Rosenberg, Suzanne
Baskar, Sivasubramanian
Glimcher, Laurie H.
Freeman, Gordon J.
Nadler, Lee M.
TITLE OF INVENTION: Tumor Cells With Increased Immunogenicity
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/261,101
FILING DATE: 30-Sep-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/966,148
FILING DATE: 27-Sep-2000
APPLICATION NUMBER: 08/147,772
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Mandragoutas, Amy E.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: RPI-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
JOURNAL: The Journal of Immunology
VOLUME: 143
ISSUE: 8
PAGES: 2714-2722
DATE: 15-OCT-1989
RELEVANT RESIDUES IN SEQ ID NO: 2: From -26 to 262
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-261-101-2

Query Match 100.0%; Score 1149; DB 15; Length 288;
Best Local Similarity 100.0%; Pred. No. 3.3e-102;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GLSHFCGVIHVTKEVATLSCGHNVSVVEELAQTRIVWQEKVKWLTMMSGDMNIWPE 60
Db 27 GLSHFCGVIHVTKEVATLSCGHNVSVVEELAQTRIVWQEKVKWLTMMSGDMNIWPE 86
Qy 61 YKRTIFDITNNLSIVILALRPSDEGTVECVLKYEKDAFKREHLAEVTLVKADPPTPS 120
Db 87 YKRTIFDITNNLSIVILALRPSDEGTVECVLKYEKDAFKREHLAEVTLVKADPPTPS 146
Qy 121 ISDFEIPSTNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 180

Db 147 ISDFEIPSTNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 206
Qy 181 NMTNHSFMCLIKYGHRLVQNTFNWNTTKQEHFPDN 216
Db 207 NMTNHSFMCLIKYGHRLVQNTFNWNTTKQEHFPDN 242

RESULT 14

US-09-910-059-131
Sequence 131, Application US/09910059
Patent No. US20020142359A1
GENERAL INFORMATION:
APPLICANT: Copley, Clive G
APPLICANT: Edge, Michael Derek
APPLICANT: Emery, Stephen Charles
TITLE OF INVENTION: Monoclonal Antibody to CEA, Conjugates Comprising Said Antibody,
TITLE OF INVENTION: Their Therapeutic use in an Adept System
FILE REFERENCE: 1991-209
CURRENT APPLICATION NUMBER: US/09/910,059
CURRENT FILING DATE: 2001-07-23
PRIOR APPLICATION NUMBER: US 09/171,945
PRIOR FILING DATE: 1998-10-29
PRIOR APPLICATION NUMBER: PCT/GB97/01165
PRIOR FILING DATE: 1997-04-29
PRIOR APPLICATION NUMBER: GB 9703103.3
PRIOR FILING DATE: 1997-02-14
PRIOR APPLICATION NUMBER: GB9609405.7
PRIOR FILING DATE: 1996-05-04
NUMBER OF SEQ ID NOS: 131
SOFTWARE: Patent in version 3.1
SEQ ID NO 131
LENGTH: 473
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: full-length human B7.1-murine ASB7 Fd fusion
US-09-910-059-131

Query Match 100.0%; Score 1149; DB 10; Length 473;
Best Local Similarity 100.0%; Pred. No. 6.4e-102;
Matches 216; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 GLSHFCGVIHVTKEVATLSCGHNVSVVEELAQTRIVWQEKVKWLTMMSGDMNIWPE 60
Db 27 GLSHFCGVIHVTKEVATLSCGHNVSVVEELAQTRIVWQEKVKWLTMMSGDMNIWPE 86
Qy 61 YKRTIFDITNNLSIVILALRPSDEGTVECVLKYEKDAFKREHLAEVTLVKADPPTPS 120
Db 87 YKRTIFDITNNLSIVILALRPSDEGTVECVLKYEKDAFKREHLAEVTLVKADPPTPS 146
Qy 121 ISDFEIPSTNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 180
Db 147 ISDFEIPSTNIRRIICSTSGGFPPEPHLSWLENGEELNAINTTVSQDPETELYAVSSKLD 206
Qy 181 NMTNHSFMCLIKYGHRLVQNTFNWNTTKQEHFPDN 216
Db 207 NMTNHSFMCLIKYGHRLVQNTFNWNTTKQEHFPDN 242

RESULT 15

US-09-845-899A-3
Sequence 3, Application US/09845899A
Patent No. US20020147326A1
GENERAL INFORMATION:
APPLICANT: CHAIKIN, MARGERY ANN
APPLICANT: LYN, SALLY DOREEN PATRICIA
APPLICANT: SWEET, RAYMOND W.
APPLICANT: TRUNEH, ALEMSEGED
TITLE OF INVENTION: HEXAMERIC FUSION PROTEINS AND USES
TITLE OF INVENTION: THEREFOR
FILE REFERENCE: P50496
CURRENT APPLICATION NUMBER: US/09/845,899A

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; CURRENT FILING DATE: 2001-04-30
; PRIOR APPLICATION NUMBER: 09/202,346
; PRIOR FILING DATE: 1999-01-13
; PRIOR APPLICATION NUMBER: US 60/043,948
; PRIOR FILING DATE: 1997-02-19
; PRIOR APPLICATION NUMBER: US 60/038,915
; PRIOR FILING DATE: 1997-02-21
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 492
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
US-09-845-899A-3

Query Match      99.5%; Score 1143; DB 10; Length 492;
Best Local Similarity 100.0%; Pred. No. 2,6e-101;
Matches 215; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GLSHFCGVIHVTKEVATLSCGHNVSEELAQTRIYQKEKKMVLTMGDMNIWPE 60
Db 27 GLSHFCGVIHVTKEVATLSCGHNVSEELAQTRIYQKEKKMVLTMGDMNIWPE 86
QY 61 YKNRTIFDITNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLVKADPPTPS 120
Db 87 YKNRTIFDITNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLAEVTLVKADPPTPS 146
QY 121 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELVAVSSKLD 180
Db 147 ISDFEIPTSNIRRIICSTSGGPEPHLSWLENGEELNAINTTVSQDPETELVAVSSKLD 206
QY 181 NMTTNHSFMCILIKYGHRLRVNQTFFNMNTTKQEHFPD 215
Db 207 NMTTNHSFMCILIKYGHRLRVNQTFFNMNTTKQEHFPD 241
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Search completed: November 25, 2003, 16:51:48
Job time : 31 secs

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